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(54) **Title:** PROMOTERS FOR REGULATION OF PLANT GENE EXPRESSION

(57) **Abstract:** The invention provides a method to identify a plurality of plant promoters having specified characteristics and promoters identified by the method. Also provided are transgenic plants comprising the genes identified by the methods of the invention.

## PROMOTERS FOR REGULATION OF PLANT GENE EXPRESSION

The present invention relates generally to the field of plant molecular biology. More specifically, it relates to the regulation of gene expression in plants.

5 Manipulation of crop plants to alter and/or improve phenotypic characteristics (such as productivity or quality) requires the expression of heterologous genes in plant tissues. Such genetic manipulation relies on the availability of a means to drive and to control gene expression as required. For example, genetic manipulation relies on the availability and use of suitable promoters which are effective in plants and which regulate gene expression so as to  
10 give the desired effect(s) in the transgenic plant. It is advantageous to have the choice of a variety of different promoters so that the most suitable promoter may be selected for a particular gene, construct, cell, tissue, plant or environment. Moreover, the increasing interest in cotransforming plants with multiple plant transcription units (PTU) and the potential problems associated with using common regulatory sequences for these purposes merit having  
15 a variety of promoter sequences available.

Promoters (and other regulatory components) from bacteria, viruses, fungi and plants have been used to control gene expression in plant cells. Numerous plant transformation experiments using DNA constructs comprising various promoter sequences fused to various foreign genes (for example, bacterial marker genes) have led to the identification of useful  
20 promoter sequences. It has been demonstrated that sequences up to 500-1000 bases in most instances are sufficient to allow for the regulated expression of foreign genes. However, it has also been shown that sequences much longer than 1000 bases may have useful features which permit desirable, e.g., high, levels of gene expression in transgenic plants.

One desirable source for promoters which have different expression profiles is plant  
25 genomic DNA. Plant development is precisely coordinated and regulated through transcription and translation of different gene products in each cell. The expression level for each gene present in a cell not only reflects the physiological status of the cell, but also determines the range of different functions the cell can perform. Identification of genes expressed constitutively, in a specific cell type or tissue, or at a specific developmental stage, and the

analysis of the abundance of the corresponding gene product can provide valuable insights into basic molecular processes and identify promoters with desirable properties.

cDNA and high density oligonucleotide array technology allows analysis of mRNA transcripts of hundreds to thousands of genes in parallel (Schena et al., 1995; Chee et al., 1996; Lockhart et al., 1996; DeRisi et al., 1997; Lashkari et al., 1997). In some organisms with completed genome sequences, such as yeast, global gene expression profiling at the mRNA level becomes possible (DeRisi et al., 1997). Genome scale transcription profiling enables not only parallel monitoring of gene expression, but also a more subjective approach for gene discovery because objective selection of gene probes to be put on microarrays is not required (Lockhart and Winzeler, 2000).

Microarray technology has been successfully developed for studying gene expression in plants (Schena et al., 1995; Desprez et al., 1998; Yuan et al., 1998; Giege et al., 1998; Kehoe et al., 1999). The microarrays used in those studies were cDNA microarrays on glass slides or filter membranes (Duggan et al. 1999; Southern et al. 1999). The DNA probes often consist of DNA fragments of expression sequence tags (ESTs) from various *Arabidopsis* EST projects (i.e., Newman et al., 1994, Richmond et al., 2000, Schaffer et al., 2000). Microarrays with selected subsets of gene probes (usually in the hundreds) has been used to examine differences in gene expression during organ development (Yuan et al., 1998; Aharoni et al., 2000), and has revealed genes that are correlated or responsible for the defense response (Reymond et al., 2000).

There is, therefore, a great need in the art for the identification of novel sequences that can be used for expression of selected transgenes in economically important plants. More specifically, there is a need for the systematic identification of genes that are expressed in a particular manner, e.g., using microarray technology.

The present invention provides an isolated nucleic acid molecule (polynucleotide) having a plant nucleotide sequence that directs root-specific (i.e., preferential) transcription of a linked nucleic acid segment in a plant, e.g., a linked plant DNA comprising an open reading frame for a structural or regulatory gene. The nucleotide sequence preferably is obtained or isolatable from plant genomic DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%,

e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-51 or a fragment (portion) thereof (i.e., a promoter isolatable from any one of SEQ ID NOs: 1-51) or to a polypeptide encoded by an *Oryza* gene comprising SEQ ID NO: 825 or 843 or a fragment (portion) thereof (i.e., a promoter isolatable from SEQ ID NO: 825 or 843) which directs root-specific transcription of a linked nucleic acid segment. Preferred root-specific promoters comprise DNA obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs: 518-526 and 536-544 (which are promoters corresponding to a gene comprising an open reading frame having one of SEQ ID NOs: 358-366), but preferably any one of SEQ ID NOs: 536, 537, and 539-54 or a fragment thereof which directs root-specific transcription.

Also preferred are root-specific promoters comprising DNA obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising an open reading frame having any one of SEQ ID NOs: 358-366, or a fragment thereof which directs root-specific transcription, or to a polypeptide encoded by an *Oryza* gene comprising an open reading frame having SEQ ID NO: 774 or 792, or a fragment thereof which directs root-specific transcription.

The present invention also provides an isolated nucleic acid molecule having a plant nucleotide sequence that directs constitutive transcription of a linked nucleic acid segment in a host cell, e.g., a plant cell. The nucleotide sequence preferably is obtained or isolatable from plant genomic DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%,



86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs: 52-339 or a fragment thereof (i.e., a promoter isolatable from any one of SEQ ID NOs:52-339) which directs constitutive transcription of a linked nucleic acid segment, or to a polypeptide encoded by an *Oryza* gene comprising any one of SEQ ID NOs: 826-842 or 844-875 or a fragment thereof (i.e., a promoter isolatable from any one of SEQ ID NOs: 826-842, 844-875) which directs constitutive transcription of a linked nucleic acid segment. Preferred constitutive promoters comprise DNA obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene having any one of SEQ ID NOs: 477-515, 517 and 545-579 (which are promoters corresponding to a gene comprising an open reading frame having one of SEQ ID NOs:441-476 and 527-529), but preferably any one of SEQ ID NOs: 548, 550- 553, 555-558, 560, 565-568, 571-573, 575, 576, 578 and 579, or a fragment thereof which directs constitutive transcription.

Also preferred are constitutive promoters comprising DNA obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising an open reading frame having any one of SEQ ID NOs:441-476 and 527-529 or a fragment thereof which directs constitutive transcription, or to a polypeptide encoded by an *Oryza* gene comprising an open reading frame having any one of SEQ ID NOs:775-791 or 793-824 or a fragment thereof which directs constitutive transcription.

The present invention further provides an isolated nucleic acid molecule which comprises a plant nucleotide sequence that directs leaf-specific (i.e., preferential) transcription of a linked nucleic acid segment in a plant. The nucleotide sequence preferably is obtained or isolatable from plant genomic DNA. In particular, the nucleotide sequence is obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has

at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising any one of SEQ ID NOs: 693-773 or a fragment thereof (i.e.,  
 5 isolatable from any one of SEQ ID NOs:693-773) which directs leaf-specific transcription of a linked nucleic acid segment.

Preferred are leaf specific promoters comprising DNA obtained or isolatable from a gene encoding a polypeptide which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%,  
 10 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide encoded by an *Arabidopsis* gene comprising an open reading frame having any one of SEQ ID NOs:601-692 or a fragment thereof which directs leaf-specific transcription.

The invention also provides uses for an isolated nucleic acid molecule, e.g., DNA or  
 15 RNA, comprising a plant nucleotide sequence comprising an open reading frame that is preferentially expressed in leaves, roots or constitutively, and which is substantially similar, and preferably has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, amino acid sequence identity, to a polypeptide  
 20 encoded by an *Arabidopsis* gene comprising an open reading frame having any one of SEQ ID NOs:358-366, 441-476, 527-529 and 601-692 or the complement thereof, e.g., SEQ ID NOs:601-692 comprise the open reading frames corresponding to genes having promoters having one of SEQ ID NOs:693-773, or to a polypeptide encoded by an *Oryza* gene comprising an open reading frame having any one of SEQ ID NOs:774-824 or the complement  
 25 thereof. For example, root-specific DNA having open reading frames which encode peroxidases, transport proteins, defense-related proteins, proteins involved in metabolism and DNA binding proteins, and constitutive open reading frames which encode cell cycle proteins, ribosomal proteins, transcription factors, defense-related proteins, stress-related proteins, transport protein, membrane proteins, structural proteins, proteins involved in metabolism,  
 30 signaling proteins, kinases and synthases, may be useful to prepare plants that over- or underexpress the encoded product or to prepare knockout plants. Also provided are nucleic

acid molecules comprising a nucleotide sequence having an open reading frame comprising SEQ ID NO:457, 476, or 527 (constitutive) or SEQ ID NO:602, 604, 609-610 (leaf). These sequences, while being useful to over- or underexpress the encoded product, or prepare knockout plants, may be used as a control for genes that are constitutively expressed or in a leaf-specific manner.

The promoters and open reading frames of the invention can be identified by employing an array of nucleic acid samples, e.g., each sample having a plurality of oligonucleotides, and each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid expressed in, for example, one or more plant tissues and/or at one or more developmental stages, or probes corresponding to nucleic acid expressed in the cells of the leaves or root of a plant relative to control nucleic acid from cellular sources other than leaves or root. Thus, genes that are upregulated or downregulated in the majority of tissues at a majority of developmental stages, or upregulated or downregulated in one tissue such as in root or in leaves, can be systematically identified.

As described herein, GeneChip® technology was utilized to discover genes that are preferentially (or exclusively) expressed in various tissues including root and leaf, as well as those that are constitutively expressed, using labeled cRNA probes, determining expression levels by laser scanning and generally selecting for expression levels that were > 2 fold over the control. The *Arabidopsis* oligonucleotide probe array consists of probes from about 8,100 unique *Arabidopsis* genes, which covers approximately one third of the genome. This genome array permits a broader, more complete and less biased analysis of gene expression. Using this approach, 51 genes were identified, the expression of which was altered, e.g., elevated, in root tissues, and 92 genes were identified, the expression of which was altered at least 4-fold in leaf tissue. Similarly, 288 genes were identified that were constitutively expressed.

Generally, the promoters of the invention may be employed to express an open reading frame from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, or an environment or stress resistance gene, i.e., one or more genes that confer herbicide resistance

or tolerance, insect resistance or tolerance, disease resistance or tolerance (viral, bacterial, fungal, oomycete, or nematode), stress tolerance or resistance (as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress, or oxidative stress), increased yields, food content and makeup, physical appearance, male sterility, drydown, standability, prolificacy, starch properties or quantity, oil quantity and quality, amino acid or protein composition, and the like. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of agent administration, infection with a pathogen, or exposure to stress. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism.

In particular, root-specific promoters may be useful for expressing defense-related genes, including those conferring insecticidal resistance and stress tolerance genes, e.g., salt, cold or drought tolerance, and genes for altering nutrient uptake, and leaf-specific promoters may be useful for producing large quantities of protein, for expressing oils or proteins of interest, genes for increasing the nutritional value of a plant, and for expressing defense-related genes (e.g., against pathogens such as a virus or fungus), including genes encoding insecticidal polypeptides. Constitutive promoters are useful for expressing a wide variety of genes including those which alter metabolic pathways, confer disease resistance, for protein production, e.g., antibody production, or to improve nutrient uptake. Constitutive promoters may be modified so as to be regulatable, e.g., inducible. The genes and promoters described hereinabove can be used to identify orthologous genes and their promoters which are also likely expressed in a particular tissue and/or development manner. Moreover, the orthologous promoters are useful to express linked open reading frames. In addition, by aligning the promoters of these orthologs, novel *cis* elements can be identified that are useful to generate synthetic promoters.

Hence, the isolated nucleic acid molecules of the invention include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleotide sequences in organisms other than *Arabidopsis*, including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat, rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, tobacco, sugarbeet, or rice. An orthologous gene is a gene from a different species that encodes a product having the same or

similar function, e.g., catalyzing the same reaction as a product encoded by a gene from a reference organism. Thus, an ortholog includes polypeptides having less than, e.g., 65% amino acid sequence identity, but which ortholog encodes a polypeptide having the same or similar function. Databases such GenBank or one found at <http://bioserver.myongjiac.kr/rjce.html> (for rice) may be employed to identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice, wheat, sunflower or alfalfa. SEQ ID NOs:598-600, for example, are the rice promoter, open reading frame and amino acid sequence for rice polyubiquitin, the ortholog of the *Arabidopsis* gene comprising SEQ ID NO:155. For example, SEQ ID NOs:774 and 792 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:360; SEQ ID NOs:789-790, 799, and 813 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:441; SEQ ID NOs: 781, 804-805, 810, 816-817, and 822 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:442; SEQ ID NOs:777, 782-783, 806, and 820 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:443; SEQ ID NOs:791, 793, and 808 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:446; SEQ ID NO:795 is a rice ortholog of the *Arabidopsis* gene comprising SEQ ID NO:449; SEQ ID NOs:776, 784, 787, 800, and 807 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:450; SEQ ID NO:779 is a rice ortholog of the *Arabidopsis* gene comprising SEQ ID NO:451; SEQ ID NO:803 is a rice ortholog of the *Arabidopsis* gene comprising SEQ ID NO:454; SEQ ID NOs:788 is a rice ortholog of the *Arabidopsis* gene comprising SEQ ID NO:458; SEQ ID NO:786 is a rice ortholog of the *Arabidopsis* gene comprising SEQ ID NO:465; SEQ ID NOs:775, 778, and 814-815 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:466; SEQ ID NOs:785 and 798 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:467; SEQ ID NOs:794, 809, 812 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:471; SEQ ID NO:797 is a rice ortholog of the *Arabidopsis* gene comprising SEQ ID NO:472; SEQ ID NOs:780, 796, 802, 819, 821, and 823 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:527; SEQ ID NOs:811 and 824 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:528; and SEQ ID NOs:801 and 818 are rice orthologs of the *Arabidopsis* gene comprising SEQ ID NO:529 (Table 14). Additional orthologs of *Arabidopsis* genes herein are identified herein, such as rice orthologs for SEQ ID NOs:359-360, 441-443, 446-447, 449-450, 465-467 and 527-529; corn orthologs for SEQ ID NOs:360, 441-442, 465-467, 527, 529; wheat

orthologs for SEQ ID NOs:441-442; sunflower orthologs for SEQ ID NOs:441-442; and alfalfa orthologs for SEQ ID NOs:365 and 529 (Table 15). Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences or to clone the equivalent sequences from different *Arabidopsis* DNAs.

5 The encoded ortholog products likely have at least 70% sequence identity to each other. Hence, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence from a gene that encodes a polypeptide having at least 70% identity to a polypeptide encoded by a gene having one or more of the *Arabidopsis* or *Oryza* sequences disclosed herein. For example, promoter sequences within the scope of the invention are those which  
10 direct expression of an open reading frame which encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by a gene having a promoter selected from the group consisting of SEQ ID NOs:1-339, 447-515, 517-526, 536-579 and 693-773 or a polypeptide that is substantially similar to an *Oryza* polypeptide encoded by a gene having a promoter selected from the group consisting of SEQ ID NOs:825-875.

15 Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:1-339, 477-515, 517-526, 536-579, and 693-773, or the promoter orthologs thereof, e.g., SEQ ID NOs: 825-875, which include the minimal  
20 promoter region.

In a particular embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95%  
25 sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:1-339, 477-515, 517-526, 536-579, and 693-773, or the promoter orthologs thereof, which include the minimal promoter region.

30 In a preferred embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g.,

40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95% sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs: 536-579, preferably of any one of SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter orthologs thereof, which include the minimal promoter region.

Preferably, the nucleotide sequence that includes the promoter region includes at least one copy of a TATA box and, for leaf-specific expression, preferably a light responsive element, e.g., SEQ ID NO:587. Thus, the invention provides plant promoters, including orthologs of *Arabidopsis* promoters corresponding to any one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, 693-773, e.g., SEQ ID NOs:825-875 and orthologs thereof. The present invention further provides a composition, an expression cassette or a recombinant vector containing the nucleic acid molecule of the invention, and host cells comprising the expression cassette or vector, e.g., comprising a plasmid. In particular, the present invention provides an expression cassette or a recombinant vector comprising a promoter of the invention linked to a nucleic acid segment which, when present in a plant, plant cell or plant tissue, results in transcription of the linked nucleic acid segment.

In its broadest sense, the term "substantially similar" when used herein with respect to a nucleotide sequence means that the nucleotide sequence is part of a gene which encodes a polypeptide having substantially the same structure and function as a polypeptide encoded by a gene for the reference nucleotide sequence, e.g., the nucleotide sequence comprises a promoter from a gene that is the ortholog of the gene corresponding to the reference nucleotide sequence, as well as promoter sequences that are structurally related the promoter sequences particularly exemplified herein, i.e., the substantially similar promoter sequences hybridize to the complement of the promoter sequences exemplified herein under high or very high stringency conditions. The term "substantially similar" thus includes nucleotide sequences wherein the sequence has been modified, for example, to optimize expression in particular cells, as well as nucleotide sequences encoding a variant polypeptide having one or more amino acid substitutions relative to the (unmodified) polypeptide encoded by the reference sequence,

which substitution(s) does not alter the activity of the variant polypeptide relative to the unmodified polypeptide. In its broadest sense, the term "substantially similar" when used herein with respect to polypeptide means that the polypeptide has substantially the same structure and function as the reference polypeptide. The percentage of amino acid sequence identity between the substantially similar and the reference polypeptide is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, wherein the reference polypeptide is an *Arabidopsis* polypeptide encoded by a gene with a promoter having any one of SEQ ID NOs:1-339, 477-515, 517-526, 536-579, and 693-773, e.g., a nucleotide sequence comprising an open reading frame having any one of SEQ ID NOs: 358-366, 441-476, 527-529 or 601-692, or wherein the reference polypeptide is an *Oryza* polypeptide encoded by a gene with a promoter having any one of SEQ ID NOs:825-875. One indication that two polypeptides are substantially similar to each other, besides having substantially the same function, is that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

Sequence comparisons maybe carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www.hto.usc.edu/software/seqaln/index.html>). The localS program, version 1.16, is preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

The invention also provides sense and anti-sense nucleic acid molecules corresponding to the open reading frames identified herein as well as their orthologs. Also provided are



compositions, expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule which comprises a nucleic acid segment which encodes a polypeptide which is preferentially expressed in leaves or roots (e.g., SEQ ID NOs:358-366, 441-476, 527-529, 774, 729 and 601-692), or constitutively expressed, in either sense or antisense orientation.

In one embodiment, the invention provides an expression cassette or vector containing an isolated nucleic acid molecule having a nucleotide sequence that directs root-specific, constitutive, or leaf-specific transcription of a linked nucleic acid segment in a cell, which nucleotide sequence is from a gene which encodes a polypeptide having, e.g., at least 70% identity to an *Arabidopsis* polypeptide encoded by a gene having one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579 or 693-773, preferably one of SEQ ID NOs: 536-579, more preferably one of SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter orthologs thereof, e.g., SEQ ID NOs:825-875, and which nucleotide sequence is optionally operably linked to other suitable regulatory sequences, e.g., a transcription terminator sequence, operator, repressor binding site, transcription factor binding site and/or an enhancer. This expression cassette or vector may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette may be operatively linked to a structural gene, the open reading frame thereof, or a portion thereof. The expression cassette may further comprise a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell or protoplast. Further, the expression cassette or vector can be contained in a transformed plant or cells thereof, and the plant may be a dicot or a monocot. In particular, the plant may be a cereal plant.

The present invention further provides a method of augmenting a plant genome by contacting plant cells with a nucleic acid molecule of the invention, e.g., one having a nucleotide sequence that directs root-specific, constitutive or leaf-specific transcription of a linked nucleic acid segment isolatable or obtained from a plant gene encoding a polypeptide that is substantially similar to a polypeptide encoded by the an *Arabidopsis* gene having a sequence according to any one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, or 693-773, preferably to any one of SEQ ID NOs: 536-579, more preferably to any one of SEQ ID Nos: 536; 537; 539-542;

548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter orthologs thereof, e.g., SEQ ID NOs:825-875, so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the nucleic acid molecule in the cells of the plant.

5 The nucleic acid molecule may be present in the nucleus, chloroplast, mitochondria and/or plastid of the cells of the plant. The present invention also provides a transgenic plant prepared by this method, a seed from such a plant and progeny plants from such a plant including hybrids and inbreds. Preferred transgenic plants are transgenic maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat, rye,  
10 turfgrass, millet, sugarcane, tomato, or potato.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields and/or produce a  
15 better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one  
20 lacking the particular nucleic acid molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule  
25 inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these crossed fertile transgenic plants.

The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting  
30 appropriate progeny plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to

hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome  
5 of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic plants according to the invention can be used for the breeding of improved plant lines that for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be  
10 obtained that, due to their optimized genetic "equipment", yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions.

The present invention also provides a method to identify a nucleotide sequence that directs root-specific transcription of linked nucleic acid in the genome of a plant cell by  
15 contacting a probe of plant nucleic acid, e.g., cRNA, isolated from root as well as other tissues of a plant, with a plurality of isolated nucleic acid samples on one or more, i.e., a plurality of, solid substrates so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Each sample comprises one or a plurality of oligonucleotides corresponding to at least a  
20 portion of a plant gene. Then complex formation is compared between samples contacted with the root-specific probe and samples contacted with a non-root specific probe so as to determine which RNAs are expressed in root tissues of the plant. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

The present invention also provides a method to identify a nucleotide sequence that  
25 directs constitutive transcription of nucleic acid in the genome of a plant cell by contacting a probe of plant nucleic acid, e.g., cRNA, isolated from various tissues of a plant and at various developmental stages with a plurality of isolated nucleic acid samples on one or more, i.e., a plurality of, solid substrates so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in  
30 the probe. Each sample comprises one or a plurality of oligonucleotides corresponding to at least a portion of a plant gene. Complex formation is then compared to determine which

RNAs are present in a majority of, preferably in substantially all, tissues, in a majority of, preferably at substantially all, developmental stages of the plant. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

The invention also provides a gene, the expression of which is useful to normalize the expression of other genes. When performing gene expression quantitative analysis, it is important to normalize the gene expression of the unknown to a known constitutive expressing gene. To achieve accurate relative quantification for the measurement of gene expression in samples, the expression of the gene of interest is compared to the expression of a gene whose expression does not vary with experimental treatment. This comparison is essential for accurate relative quantification because this normalization process eliminates any remaining error that may arise from sample quality variance. Using methodologies described herein, two genes were identified, APX3 and TRX3 (ascorbate peroxidase and thioredoxin), whose expression does not vary upon virus infection, bacterial infection or between different tissue types. Probes and primer sets were prepared to measure the expression levels of these genes using quantitative PCR. Whereas the expression level of a pathogenesis related gene in infected *Arabidopsis* rises upon infection compared to the same gene in the noninfected control plant, the expression levels of APX3 and TRX3 remained consistent in mock and experimentally treated plants. APX3 and TRX3 gene expression levels also remained consistent between normal and cold-treated plants. These genes and their plant kingdom orthologs are useful as normalization standards for quantitative gene expression analysis in *Arabidopsis*, as well as other dicots and monocots.

The present invention also provides a method to identify a nucleotide sequence that directs transcription of nucleic acid in the genome of a plant cell in leaf tissue, by contacting a probe of plant nucleic acid, e.g., cRNA, isolated from leaf as well as other tissues of a plant with a plurality of isolated nucleic acid samples on one or more, i.e., a plurality of, solid substrates, so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Each sample comprises one or a plurality of, oligonucleotides corresponding to at least a portion of a plant gene. Then complex formation is determined or detected to identify which samples

represent genes that are expressed in leaf. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

The compositions of the invention include plant nucleic acid molecules, and the amino acid sequences for the polypeptides or partial-length polypeptides encoded by the nucleic acid molecule which comprises an open reading frame. These sequences can be employed to alter expression of a particular gene corresponding to the open reading frame by decreasing or eliminating expression of that plant gene or by overexpressing a particular gene product. Methods of this embodiment of the invention include stably transforming a plant with the nucleic acid molecule which includes an open reading frame operably linked to a promoter capable of driving expression of that open reading frame (sense or antisense) in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule which comprises an open reading frame or a fragment thereof encoding a partial-length polypeptide having the activity of the full length polypeptide, is meant a sequence having at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. Thus, to express a particular gene product, the method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a promoter linked to an open reading frame so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant or cells thereof preferably expresses the open reading frame in an amount that alters the amount of the gene product in the plant or cells thereof, which product is encoded by the open reading frame. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under stringent conditions with a nucleic acid molecule of the invention as well as RNA which is transcribed from the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support

and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

A computer readable medium containing one or more of the nucleotide sequences of the invention as well as methods of use for the computer readable medium are provided. This medium allows a nucleotide sequence corresponding to at least one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, 693-773 or 825-875 (promoters), and 358-366, 441-476, 527-529, 601-692 or 774-824 (open reading frames), to be used as a reference sequence to search against a database. This medium also allows for computer-based manipulation of a nucleotide sequence corresponding to at least one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, 693-773 or 825-875 and 358-366, 441-476, 527-529, 601-692 or 774-824.

In accordance with the present invention, nucleic acid constructs are provided that allow initiation of transcription in a "root-specific" or "leaf-specific" manner. Constructs of the invention comprise regulated transcription initiation regions associated with protein translation elongation, and the compositions of the present invention are drawn to novel nucleotide sequences for root-specific as well as leaf-specific expression. The present invention thus provides for isolated nucleic acid molecules comprising a plant nucleotide sequence that directs root-specific or leaf-specific transcription of a linked nucleic acid fragment in a plant cell. Preferably, nucleotide sequence is obtained from plant genomic DNA from a gene encoding a polypeptide which is substantially similar and preferably has, e.g., at least 70% amino acid sequence identity to a polypeptide encoded by an *Arabidopsis* gene having any one of SEQ ID NOs: 1-51, 518-526 and 536-544 (root-specific promoters) or orthologs thereof, e.g., SEQ ID Nos: 825 or 843, or 693-773 (leaf-specific promoters) or a fragment thereof which directs root- or leaf-specific expression, respectively. Thus, these nucleotide sequences exhibit promoter activity in root or leaf tissues. Root-specific or leaf-specific promoters may be obtained from other plant species by using the *Arabidopsis* promoter or corresponding genes sequences described herein as probes to screen for

homologous structural genes in other plants by hybridization under low, moderate or stringent hybridization conditions. Regions of the tissue-specific promoter sequences of the present invention which are conserved among species could also be used as PCR primers to amplify a segment from a species other than *Arabidopsis*, and that segment used as a hybridization probe (the latter approach permitting higher stringency screening) or in a transcriptional assay to determine promoter activity. Moreover, the tissue-specific sequences could be employed to identify structurally related sequences in a database using computer algorithms.

These promoters are capable of driving the expression of a coding sequence in a target cell, particularly in a plant cell. The promoter sequences and methods disclosed herein are useful in regulating tissue-specific expression of any heterologous nucleotide sequence in a host plant in order to vary the phenotype of that plant. These promoters can be used with combinations of enhancer, upstream elements, and/or activating sequences from the 5' flanking regions of plant expressible structural genes. Similarly the upstream element can be used in combination with various plant promoter sequences.

Also in accordance with the present invention, nucleic acid constructs are provided that allow initiation of transcription in a "tissue-independent," "tissue general," or "constitutive" manner. Constructs of this embodiment invention comprise regulated transcription initiation regions associated with protein translation elongation and the compositions of this embodiment of the present invention are drawn to novel nucleotide sequences for tissue-independent, tissue-general, or constitutive plant promoters. By "tissue-independent," "tissue-general," or "constitutive" is intended expression in the cells throughout a plant at most times and in most tissues. As with other promoters classified as "constitutive" (e.g., ubiquitin), some variation in absolute levels of expression can exist among different tissues or stages.

The present invention thus provides for isolated nucleic acid molecules comprising a plant nucleotide sequence that directs constitutive transcription of a linked nucleic acid fragment in a plant cell. Preferably, the nucleotide sequence is obtained from plant genomic DNA from a gene encoding a polypeptide which is substantially similar and preferably has, e.g. at least 70% amino acid sequence identity to a polypeptide encoded by an *Arabidopsis* gene having any one of SEQ ID NOs:52-339, 477-515, 517, 545-579, 826-842, 844-875 or a fragment thereof which exhibits promoter activity in a constitutive fashion (i.e., at most times and in most tissues). Constitutive promoter sequences may be obtained from other plant

species by using the constitutive *Arabidopsis* promoter sequences or corresponding genes described herein as probes to screen for homologous structural genes in other plants by hybridization under low, moderate or stringent hybridization conditions. Regions of the constitutive promoter sequences of the present invention which are conserved among species  
5 could also be used as PCR primers to amplify a segment from a species other than *Arabidopsis*, and that segment used as a hybridization probe (the latter approach permitting higher stringency screening) or in a transcription assay to determine promoter activity. Moreover, the constitutive promoter sequences could be employed to identify structurally related sequences in a database using computer algorithms.

10 These constitutive promoters are capable of driving the expression of a coding sequence in a target cell, particularly in a plant cell. The promoter sequences and methods disclosed herein are useful in regulating constitutive expression of any heterologous nucleotide sequence in a host plant in order to vary the phenotype of that plant. These promoters can be used with combinations of enhancer, upstream elements, and/or activating sequences from the  
15 5' flanking regions of plant expressible structural genes. Similarly the upstream element can be used in combination with various plant promoter sequences. In one embodiment the promoter and upstream element are used together to obtain at least 10-fold higher expression of an introduced gene in monocot transgenic plants than is obtained with the maize ubiquitin 1 promoter.

20 In particular, all of the promoters of the invention are useful to modify the phenotype of a plant. Various changes in the phenotype of a transgenic plant are desirable, i.e., modifying the fatty acid composition in a plant, altering the amino acid content of a plant, altering a plant's pathogen defense mechanism, and the like. These results can be achieved by providing expression of heterologous products or increased expression of endogenous products in plants.  
25 Alternatively, the results can be achieved by providing for a reduction of expression of one or more endogenous products, particularly enzymes or cofactors in the plant. These changes result in an alteration in the phenotype of the transformed plant.

#### Definitions

30 The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences



required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA or functional RNA, or encodes a specific protein, and which includes regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

The term "native" or "wild type" gene refers to a gene that is present in the genome of an untransformed cell, i.e., a cell not having a known mutation.

A "marker gene" encodes a selectable or screenable trait.

The term "chimeric gene" refers to any gene that contains 1) DNA sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for example, genes that are either heterologous or homologous to the genes of a particular plant to be transformed.

Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host organism but that is introduced by gene transfer.

An "oligonucleotide" corresponding to a nucleotide sequence of the invention, e.g., for use in probing or amplification reactions, may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16 to 24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

The nucleotide sequences of the invention can be introduced into any plant. The genes to be introduced can be conveniently used in expression cassettes for introduction and expression in any plant of interest. Such expression cassettes will comprise the transcriptional initiation region of the invention linked to a nucleotide sequence of interest. Preferred promoters include constitutive, tissue-specific, developmental-specific, inducible and/or viral promoters. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes. The cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase

catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without  
5 introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or  
10 stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters.

15 "5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a  
20 coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.

25 The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

30 The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of

an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

5           The term "intracellular localization sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and  
10 causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding  
15 sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that  
20 includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to  
25 enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements  
30 derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of

protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e., further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the open reading frame (ORF) that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of  $\geq 1\%$  of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and includes both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al. (1989). Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the

tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysone-inducible systems.

5 "Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully  
10 differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic  
15 acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can  
20 be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene, ORF or portion thereof, or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA.  
25 Expression may also refer to the production of protein.

"Specific expression" is the expression of gene products which is limited to one or a few plant tissues (spatial limitation) and/or to one or a few plant developmental stages (temporal limitation). It is acknowledged that hardly a true specificity exists: promoters seem to be preferably switch on in some tissues, while in other tissues there can be no or only little  
30 activity. This phenomenon is known as leaky expression. However, with specific expression in this invention is meant preferable expression in one or a few plant tissues.

The "expression pattern" of a promoter (with or without enhancer) is the pattern of expression levels which shows where in the plant and in what developmental stage transcription is initiated by said promoter. Expression patterns of a set of promoters are said to be complementary when the expression pattern of one promoter shows little overlap with the expression pattern of the other promoter. The level of expression of a promoter can be determined by measuring the 'steady state' concentration of a standard transcribed reporter mRNA. This measurement is indirect since the concentration of the reporter mRNA is dependent not only on its synthesis rate, but also on the rate with which the mRNA is degraded. Therefore, the steady state level is the product of synthesis rates and degradation rates.

The rate of degradation can however be considered to proceed at a fixed rate when the transcribed sequences are identical, and thus this value can serve as a measure of synthesis rates. When promoters are compared in this way techniques available to those skilled in the art are hybridization S1-RNase analysis, northern blots and competitive RT-PCR. This list of techniques in no way represents all available techniques, but rather describes commonly used procedures used to analyze transcription activity and expression levels of mRNA.

The analysis of transcription start points in practically all promoters has revealed that there is usually no single base at which transcription starts, but rather a more or less clustered set of initiation sites, each of which accounts for some start points of the mRNA. Since this distribution varies from promoter to promoter the sequences of the reporter mRNA in each of the populations would differ from each other. Since each mRNA species is more or less prone to degradation, no single degradation rate can be expected for different reporter mRNAs. It has been shown for various eukaryotic promoter sequences that the sequence surrounding the initiation site ('initiator') plays an important role in determining the level of RNA expression directed by that specific promoter. This includes also part of the transcribed sequences. The direct fusion of promoter to reporter sequences would therefore lead to suboptimal levels of transcription.

A commonly used procedure to analyze expression patterns and levels is through determination of the 'steady state' level of protein accumulation in a cell. Commonly used candidates for the reporter gene, known to those skilled in the art are  $\beta$ -glucuronidase (GUS),

chloramphenicol acetyl transferase (CAT) and proteins with fluorescent properties, such as green fluorescent protein (GFP) from *Aequora victoria*. In principle, however, many more proteins are suitable for this purpose, provided the protein does not interfere with essential plant functions. For quantification and determination of localization a number of tools are suited. Detection systems can readily be created or are available which are based on, e.g., immunochemical, enzymatic, fluorescent detection and quantification. Protein levels can be determined in plant tissue extracts or in intact tissue using *in situ* analysis of protein expression.

Generally, individual transformed lines with one chimeric promoter reporter construct will vary in their levels of expression of the reporter gene. Also frequently observed is the phenomenon that such transformants do not express any detectable product (RNA or protein). The variability in expression is commonly ascribed to 'position effects', although the molecular mechanisms underlying this inactivity are usually not clear.

The term "average expression" is used here as the average level of expression found in all lines that do express detectable amounts of reporter gene, so leaving out of the analysis plants that do not express any detectable reporter mRNA or protein.

"Root expression level" indicates the expression level found in protein extracts of complete plant roots. Likewise, leaf, and stem expression levels, are determined using whole extracts from leaves and stems. It is acknowledged however, that within each of the plant parts just described, cells with variable functions may exist, in which promoter activity may vary.

"Non-specific expression" refers to constitutive expression or low level, basal ('leaky') expression in undesired cells or tissues from a 'regulated promoter'.

"Altered levels" refers to the level of expression in transgenic organisms that differs from that of normal or untransformed organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed (nontransgenic) cells or organisms.

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.



"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

5 "Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al. 1998).

10 "Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

The terms "heterologous DNA sequence," "exogenous DNA segment" or  
15 "heterologous nucleic acid," as used herein, each refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA  
20 sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides. A "homologous" DNA sequence is a DNA sequence that is naturally associated with a host cell into which it is introduced.

25 "Homologous to" in the context of nucleotide sequence identity refers to the similarity between the nucleotide sequence of two nucleic acid molecules or between the amino acid sequences of two protein molecules. Estimates of such homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (as described in Haines and Higgins (eds.), Nucleic Acid  
30 Hybridization, IRL Press, Oxford, U.K.), or by the comparison of sequence similarity between two nucleic acids or proteins.

The term "substantially similar" refers to nucleotide and amino acid sequences that represent functional and/or structural equivalents of *Arabidopsis* sequences disclosed herein. For example, altered nucleotide sequences which simply reflect the degeneracy of the genetic code but nonetheless encode amino acid sequences that are identical to a particular amino acid sequence are substantially similar to the particular sequences. In addition, amino acid sequences that are substantially similar to a particular sequence are those wherein overall amino acid identity is at least 65% or greater to the instant sequences. Modifications that result in equivalent nucleotide or amino acid sequences are well within the routine skill in the art. Moreover, the skilled artisan recognizes that equivalent nucleotide sequences encompassed by this invention can also be defined by their ability to hybridize, under low, moderate and/or stringent conditions (e.g., 0.1X SSC, 0.1% SDS, 65°C), with the nucleotide sequences that are within the literal scope of the instant claims.

"Target gene" refers to a gene on the replicon that expresses the desired target coding sequence, functional RNA, or protein. The target gene is not essential for replicon replication. Additionally, target genes may comprise native non-viral genes inserted into a non-native organism, or chimeric genes, and will be under the control of suitable regulatory sequences. Thus, the regulatory sequences in the target gene may come from any source, including the virus. Target genes may include coding sequences that are either heterologous or homologous to the genes of a particular plant to be transformed. However, target genes do not include native viral genes. Typical target genes include, but are not limited to genes encoding a structural protein, a seed storage protein, a protein that conveys herbicide resistance, and a protein that conveys insect resistance. Proteins encoded by target genes are known as "foreign proteins". The expression of a target gene in a plant will typically produce an altered plant trait.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

"Transcription Stop Fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Replication gene" refers to a gene encoding a viral replication protein. In addition to the ORF of the replication protein, the replication gene may also contain other overlapping or non-overlapping ORF(s), as are found in viral sequences in nature. While not essential for replication, these additional ORFs may enhance replication and/or viral DNA accumulation. Examples of such additional ORFs are AC3 and AL3 in ACMV and TGMV geminiviruses, respectively.

"Chimeric *trans*-acting replication gene" refers either to a replication gene in which the coding sequence of a replication protein is under the control of a regulated plant promoter other than that in the native viral replication gene, or a modified native viral replication gene, for example, in which a site specific sequence(s) is inserted in the 5' transcribed but untranslated region. Such chimeric genes also include insertion of the known sites of replication protein binding between the promoter and the transcription start site that attenuate transcription of viral replication protein gene.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

"*Trans*-activation" refers to switching on of gene expression or replicon replication by the expression of another (regulatory) gene in *trans*.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of

transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al. 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

5 "Transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995 and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods  
10 using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

15 "Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

20 "Transient expression" refers to expression in cells in which a virus or a transgene is introduced by viral infection or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive  
25 generations.

"Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

30 "Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles.

They may be derived by self-fertilization of primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Wild-type" refers to a virus or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

5       The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are  
10       metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is  
15       substituted with mixed-base and/or deoxyinosine residues (Batzner et al., 1991; Ohtsuka et al., 1985; Rossolini et al. 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be  
20       single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid" or "nucleic acid sequence" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

      The invention encompasses isolated or substantially purified nucleic acid or protein  
25       compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an  
30       "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by

recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein of interest chemicals.

The nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant (variant) forms. Such variants will continue to possess the desired activity, i.e., either promoter activity or the activity of the product encoded by the open reading frame of the non-variant nucleotide sequence.

Thus, by "variants" is intended substantially similar sequences. For nucleotide sequences comprising an open reading frame, variants include those sequences that, because of the degeneracy of the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis and for open reading frames, encode the native protein, as well as those that encode a polypeptide having amino acid substitutions relative to the native protein. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g., 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98% and 99% nucleotide sequence identity to the native (wild type or endogenous) nucleotide sequence.

“Conservatively modified variations” of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded protein. Such nucleic acid variations are “silent variations” which are one species of “conservatively modified variations.” Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each “silent variation” of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

The nucleic acid molecules of the invention can be “optimized” for enhanced expression in plants of interest. See, for example, EPA 035472; WO 91/16432; Perlak et al., 1991; and Murray et al., 1989. In this manner, the open reading frames in genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Cramer et al., 1997; Moore et al., 1997; Zhang et al., 1997; Cramer et al., 1998; and U.S. Patent Nos. 5,605,793 and 5,837,458.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites  
5 in the native protein. Such variants may result from, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can  
10 be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U. S. Patent No. 4,873,192; Walker and Gaastra, 1983 and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff et al. (1978). Conservative substitutions, such  
15 as exchanging one amino acid with another having similar properties, are preferred.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution  
20 tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine  
25 (N), Glutamine (Q). See also, Creighton, 1984. In addition, individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a  
30 promoter operably linked to the nucleotide sequence of interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the



nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

Preferably the nucleic acid in the vector is under the control of, and operably linked to, an appropriate promoter or other regulatory elements for transcription in a host cell such as a microbial, e.g. bacterial, or plant cell. The vector may be a bi-functional expression vector which functions in multiple hosts. In the case of genomic DNA, this may contain its own promoter or other regulatory elements and in the case of cDNA this may be under the control of an appropriate promoter or other regulatory elements for expression in the host cell.

"Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector.

Marker genes typically include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

5 "Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds, tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The following terms are used to describe the sequence relationships between two or  
10 more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete  
15 cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two  
20 sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus,  
25 the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al. 1981; the homology alignment algorithm of Needleman and Wunsch 1970; the search-for-similarity-method of Pearson and Lipman 1988; the algorithm of Karlin and Altschul, 1990, modified as  
30 in Karlin and Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from 5 Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al. 1988; Higgins et al. 1989; Corpet et al. 1988; Huang et al. 1992; and Pearson et al. 1994. The ALIGN program is based on the 10 algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in 15 the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment 20 score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, 25 the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum 30 probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic

acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST  
5 2.0) can be utilized as described in Altschul et al. 1997. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as  
10 defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

15 For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical  
20 nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When  
25 percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent  
30 sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have

"sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the

specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window.

Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch (1970). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s)

substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

5           "Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridization are sequence dependent, and are different under different environmental parameters. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the  
10       function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the  $T_m$  can be approximated from the equation of Meinkoth and Wahl, 1984;  $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$ ; where  $M$  is the molarity of monovalent cations,  $\%GC$  is the percentage of guanosine and cytosine nucleotides in the DNA,  $\% \text{ form}$  is the percentage of formamide in  
15       the hybridization solution, and  $L$  is the length of the hybrid in base pairs.  $T_m$  is reduced by about  $1^\circ\text{C}$  for each 1% of mismatching; thus,  $T_m$ , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with  $>90\%$  identity are sought, the  $T_m$  can be decreased  $10^\circ\text{C}$ . Generally, stringent conditions are selected to be about  $5^\circ\text{C}$  lower than the thermal melting point  $T_m$  for the specific sequence and  
20       its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or  $4^\circ\text{C}$  lower than the thermal melting point  $T_m$ ; moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or  $10^\circ\text{C}$  lower than the thermal melting point  $T_m$ ; low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or  $20^\circ\text{C}$  lower than the thermal melting point  $T_m$ . Using the  
25       equation, hybridization and wash compositions, and desired  $T_m$ , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a  $T_m$  of less than  $45^\circ\text{C}$  (aqueous solution) or  $32^\circ\text{C}$  (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the  
30       hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent

hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point  $T_m$  for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at 45°C for 15 minutes. An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long probes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the  $T_m$  for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide



sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO<sub>4</sub>, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

“DNA shuffling” is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may have an altered biological activity with respect to the polypeptide encoded by the template DNA.

“Recombinant DNA molecule” is a combination of DNA sequences that are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., 1989.

The word “plant” refers to any plant, particularly to seed plant, and “plant cell” is a structural and physiological unit of the plant, which comprises a cell wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

“Significant increase” is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

“Significantly less” means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

Virtually any DNA composition may be used for delivery to recipient plant cells, e.g., monocotyledonous cells, to ultimately produce fertile transgenic plants in accordance with the

present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instances containing only the DNA element to be expressed in the plant, and the like, may be employed. The construction of vectors which may be employed in conjunction with the present invention will be known to those of skill of the art in light of the present disclosure (see, e.g., Sambrook et al., 1989; Gelvin et al., 1990).

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

In certain embodiments, it is contemplated that one may wish to employ replication-competent viral vectors in monocot transformation. Such vectors include, for example, wheat dwarf virus (WDV) "shuttle" vectors, such as pW1-11 and PW1-GUS (Ugaki et al., 1991). These vectors are capable of autonomous replication in maize cells as well as *E. coli*, and as such may provide increased sensitivity for detecting DNA delivered to transgenic cells. A replicating vector may also be useful for delivery of genes flanked by DNA sequences from transposable elements such as Ac, Ds, or Mu. It has been proposed (Laufs et al., 1990) that transposition of these elements within the maize genome requires DNA replication. It is also contemplated that transposable elements would be useful for introducing DNA fragments lacking elements necessary for selection and maintenance of the plasmid vector in bacteria, e.g., antibiotic resistance genes and origins of DNA replication. It is also proposed that use of a transposable element such as Ac, Ds, or Mu would actively promote integration of the desired DNA and hence increase the frequency of stably transformed cells. The use of a transposable element such as Ac, Ds, or Mu may actively promote integration of the DNA of interest and hence increase the frequency of stably transformed cells. Transposable elements may be useful to allow separation of genes of interest from elements necessary for selection

and maintenance of a plasmid vector in bacteria or selection of a transformant. By use of a transposable element, desirable and undesirable DNA sequences may be transposed apart from each other in the genome, such that through genetic segregation in progeny, one may identify plants with either the desirable or the undesirable DNA sequences.

5 DNA useful for introduction into plant cells includes that which has been derived or isolated from any source, that may be subsequently characterized as to structure, size and/or function, chemically altered, and later introduced into plants. An example of DNA "derived" from a source, would be a DNA sequence that is identified as a useful fragment within a given organism, and which is then chemically synthesized in essentially pure form. An example of  
10 such DNA "isolated" from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering. Such DNA is commonly referred to as "recombinant DNA."

Therefore useful DNA includes completely synthetic DNA, semi-synthetic DNA, DNA  
15 isolated from biological sources, and DNA derived from introduced RNA. Generally, the introduced DNA is not originally resident in the plant genotype which is the recipient of the DNA, but it is within the scope of the invention to isolate a gene from a given plant genotype, and to subsequently introduce multiple copies of the gene into the same genotype, e.g., to enhance production of a given gene product such as a storage protein or a protein that confers  
20 tolerance or resistance to water deficit.

The introduced DNA includes but is not limited to, DNA from plant genes, and non-plant genes such as those from bacteria, yeasts, animals or viruses. The introduced DNA can include modified genes, portions of genes, or chimeric genes, including genes from the same or different maize genotype. The term "chimeric gene" or "chimeric DNA" is defined as a gene  
25 or DNA sequence or segment comprising at least two DNA sequences or segments from species which do not combine DNA under natural conditions, or which DNA sequences or segments are positioned or linked in a manner which does not normally occur in the native genome of untransformed plant.

The introduced DNA used for transformation herein may be circular or linear, double-  
30 stranded or single-stranded. Generally, the DNA is in the form of chimeric DNA, such as plasmid DNA, that can also contain coding regions flanked by regulatory sequences which

promote the expression of the recombinant DNA present in the resultant plant. For example, the DNA may itself comprise or consist of a promoter that is active in a plant which is derived from a source other than that plant, or may utilize a promoter already present in a plant genotype that is the transformation target.

5        Generally, the introduced DNA will be relatively small, i.e., less than about 30 kb to minimize any susceptibility to physical, chemical, or enzymatic degradation which is known to increase as the size of the DNA increases. As noted above, the number of proteins, RNA transcripts or mixtures thereof which is introduced into the plant genome is preferably preselected and defined, e.g., from one to about 5-10 such products of the introduced DNA  
10        may be formed.

Two principal methods for the control of expression are known, viz.: overexpression and underexpression. Overexpression can be achieved by insertion of one or more than one extra copy of the selected gene. It is, however, not unknown for plants or their progeny, originally transformed with one or more than one extra copy of a nucleotide sequence, to  
15        exhibit the effects of underexpression as well as overexpression. For underexpression there are two principle methods which are commonly referred to in the art as "antisense downregulation" and "sense downregulation" (sense downregulation is also referred to as "cosuppression"). Generically these processes are referred to as "gene silencing". Both of these methods lead to an inhibition of expression of the target gene.

20        Obtaining sufficient levels of transgene expression in the appropriate plant tissues is an important aspect in the production of genetically engineered crops. Expression of heterologous DNA sequences in a plant host is dependent upon the presence of an operably linked promoter that is functional within the plant host. Choice of the promoter sequence will determine when and where within the organism the heterologous DNA sequence is expressed.

25        Furthermore, it is contemplated that promoters combining elements from more than one promoter may be useful. For example, U.S. Patent No. 5,491,288 discloses combining a Cauliflower Mosaic Virus promoter with a histone promoter. Thus, the elements from the promoters disclosed herein may be combined with elements from other promoters.

Promoters which are useful for plant transgene expression include those that are  
30        inducible, viral, synthetic, constitutive (Odell et al., 1985), temporally regulated, spatially regulated, tissue-specific, and spatio-temporally regulated.

Where expression in specific tissues or organs is desired, tissue-specific promoters may be used. In contrast, where gene expression in response to a stimulus is desired, inducible promoters are the regulatory elements of choice. Where continuous expression is desired throughout the cells of a plant, constitutive promoters are utilized. Additional regulatory sequences upstream and/or downstream from the core promoter sequence may be included in expression constructs of transformation vectors to bring about varying levels of expression of heterologous nucleotide sequences in a transgenic plant.

The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In some cases, expression in multiple tissues is desirable. While in others, tissue-specific, e.g., leaf-specific, expression is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons.

However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, spatially-regulated, chemically regulated, stress-responsive, tissue-specific, viral and synthetic promoters. Promoter sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the  $P_{tac}$  promoter can be induced to varying levels of gene expression depending on the level of isothiopropylgalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Within a plant promoter region there are several domains that are necessary for full function of the promoter. The first of these domains lies immediately upstream of the structural gene and forms the "core promoter region" containing consensus sequences,

normally 70 base pairs immediately upstream of the gene. The core promoter region contains the characteristic CAAT and TATA boxes plus surrounding sequences, and represents a transcription initiation sequence that defines the transcription start point for the structural gene.

5       The presence of the core promoter region defines a sequence as being a promoter: if the region is absent, the promoter is non-functional. Furthermore, the core promoter region is insufficient to provide full promoter activity. A series of regulatory sequences upstream of the core constitute the remainder of the promoter. The regulatory sequences determine expression level, the spatial and temporal pattern of expression and, for an important subset of promoters,  
10       expression under inductive conditions (regulation by external factors such as light, temperature, chemicals, hormones).

A range of naturally-occurring promoters are known to be operative in plants and have been used to drive the expression of heterologous (both foreign and endogenous) genes in plants: for example, the constitutive 35S cauliflower mosaic virus (CaMV) promoter, the  
15       ripening-enhanced tomato polygalacturonase promoter (Bird et al., 1988), the E8 promoter (Diekmann & Fischer, 1988) and the fruit specific 2A1 promoter (Pear et al., 1989) and many others, e.g., U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a  
20       27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea *rbcS* gene and the actin promoter from rice, e.g., the actin 2 promoter (WO 00/70067); seed specific promoters, such as the phaseolin promoter from beans, may also be used. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically  
25       regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Chemical induction of gene expression is detailed in EP 0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

30       Examples of some constitutive promoters which have been described include the rice actin 1 (Wang et al., 1992; U.S. Patent No. 5,641,876), CaMV 35S (Odell et al., 1985), CaMV 19S (Lawton et al., 1987), *nos*, *Adh*, sucrose synthase; and the ubiquitin promoters.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990) corn alcohol dehydrogenase 1 (Vogel et al., 1989; Dennis et al., 1984), corn light harvesting complex (Simpson, 1986; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985), pea small subunit RuBP carboxylase (Poulsen et al., 1986), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991),  $\alpha$ -tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), histone, and chalcone synthase promoters (Franken et al., 1991). Tissue specific enhancers are described in Fromm et al. (1989).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several other tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearyl-ACP desaturase. And fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific expression is the pea vicilin promoter (Czako et al., 1992). (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from *Arabidopsis* (Gan et al., 1995).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674. cDNA

clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in  
5 U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell  
10 protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific  
15 promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996) and Gatz (1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama et al., 1997) and  
20 ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol-(WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to environmental stress or stimuli such as increased salinity. Drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986). Accumulation of  
25 metalcarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Regulated expression of the chimeric transacting viral replication protein can be further regulated by other genetic strategies. For example, *Cre*-mediated gene activation as described  
30 by Odell et al. 1990. Thus, a DNA fragment containing 3' regulatory sequence bound by lox sites between the promoter and the replication protein coding sequence that blocks the



expression of a chimeric replication gene from the promoter can be removed by *Cre*-mediated excision and result in the expression of the *trans*-acting replication gene. In this case, the chimeric *Cre* gene, the chimeric *trans*-acting replication gene, or both can be under the control of tissue- and developmental- specific or inducible promoters. An alternate genetic strategy is the use of tRNA suppressor gene. For example, the regulated expression of a tRNA suppressor gene can conditionally control expression of a *trans*-acting replication protein coding sequence containing an appropriate termination codon as described by Ulmasov et al. 1997. Again, either the chimeric tRNA suppressor gene, the chimeric *trans*-acting replication gene, or both can be under the control of tissue- and developmental-specific or inducible promoters.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and airborne-pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the mRNA of the native DNA sequence.

To define a minimal promoter region, a DNA segment representing the promoter region is removed from the 5' region of the gene of interest and operably linked to the coding sequence of a marker (reporter) gene by recombinant DNA techniques well known to the art. The reporter gene is operably linked downstream of the promoter, so that transcripts initiating at the promoter proceed through the reporter gene. Reporter genes generally encode proteins which are easily measured, including, but not limited to, chloramphenicol acetyl transferase (CAT), beta-glucuronidase (GUS), green fluorescent protein (GFP), beta-galactosidase (beta-GAL), and luciferase.

The construct containing the reporter gene under the control of the promoter is then introduced into an appropriate cell type by transfection techniques well known to the art. To assay for the reporter protein, cell lysates are prepared and appropriate assays, which are well known in the art, for the reporter protein are performed. For example, if CAT were the  
5 reporter gene of choice, the lysates from cells transfected with constructs containing CAT under the control of a promoter under study are mixed with isotopically labeled chloramphenicol and acetyl-coenzyme A (acetyl-CoA). The CAT enzyme transfers the acetyl group from acetyl-CoA to the 2- or 3-position of chloramphenicol. The reaction is monitored by thin-layer chromatography, which separates acetylated chloramphenicol from unreacted  
10 material. The reaction products are then visualized by autoradiography.

The level of enzyme activity corresponds to the amount of enzyme that was made, which in turn reveals the level of expression from the promoter of interest. This level of expression can be compared to other promoters to determine the relative strength of the promoter under study. In order to be sure that the level of expression is determined by the  
15 promoter, rather than by the stability of the mRNA, the level of the reporter mRNA can be measured directly, such as by Northern blot analysis.

Once activity is detected, mutational and/or deletion analyses may be employed to determine the minimal region and/or sequences required to initiate transcription. Thus, sequences can be deleted at the 5' end of the promoter region and/or at the 3' end of the  
20 promoter region, and nucleotide substitutions introduced. These constructs are then introduced to cells and their activity determined.

In one embodiment, the promoter may be a gamma zein promoter, an oleosin ole16 promoter, a globulinI promoter, an actin I promoter, an actin cl promoter, a sucrose synthetase promoter, an INOPS promoter, an EXM5 promoter, a globulin2 promoter, a b-32, ADPG-  
25 pyrophosphorylase promoter, an LtpI promoter, an Ltp2 promoter, an oleosin ole17 promoter, an oleosin ole18 promoter, an actin 2 promoter, a pollen-specific protein promoter, a pollen-specific pectate lyase promoter, an anther-specific protein promoter, an anther-specific gene RTS2 promoter, a pollen-specific gene promoter, a tapetum-specific gene promoter, tapetum-specific gene RAB24 promoter, a anthranilate synthase alpha subunit promoter, an alpha zein  
30 promoter, an anthranilate synthase beta subunit promoter, a dihydrodipicolinate synthase promoter, a Thil promoter, an alcohol dehydrogenase promoter, a cab binding protein

promoter, an H3C4 promoter, a RUBISCO SS starch branching enzyme promoter, an ACCase promoter, an actin3 promoter, an actin7 promoter, a regulatory protein GF14-12 promoter, a ribosomal protein L9 promoter, a cellulose biosynthetic enzyme promoter, an S-adenosyl-L-homocysteine hydrolase promoter, a superoxide dismutase promoter, a C-kinase receptor promoter, a phosphoglycerate mutase promoter, a root-specific RCc3 mRNA promoter, a glucose-6 phosphate isomerase promoter, a pyrophosphate-fructose 6-phosphatelposphotransferase promoter, an ubiquitin promoter, a beta-ketoacyl-ACP synthase promoter, a 33 kDa photosystem 11 promoter, an oxygen evolving protein promoter, a 69 kDa vacuolar ATPase subunit promoter, a metallothionein-like protein promoter, a glyceraldehyde-3-phosphate dehydrogenase promoter, an ABA- and ripening- inducible-like protein promoter, a phenylalanine ammonia lyase promoter, an adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase promoter, an  $\alpha$ - tubulin promoter, a cab promoter, a PEPCase promoter, an R gene promoter, a lectin promoter, a light harvesting complex promoter, a heat shock protein promoter, a chalcone synthase promoter, a zein promoter, a globulin-1 promoter, an ABA promoter, an auxin-binding protein promoter, a UDP glucose flavonoid glycosyl-transferase gene promoter, an NTI promoter, an actin promoter, an opaque 2 promoter, a b70 promoter, an oleosin promoter, a CaMV 35S promoter, a CaMV 19S promoter, a histone promoter, a turgor-inducible promoter, a pea small subunit RuBP carboxylase promoter, a Ti plasmid mannopine synthase promoter, Ti plasmid nopaline synthase promoter, a petunia chalcone isomerase promoter, a bean glycine rich protein I promoter, a CaMV 35S transcript promoter, a potato patatin promoter, or a S-E9 small subunit RuBP carboxylase promoter.

In addition to promoters, a variety of 5N and 3N transcriptional regulatory sequences are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA polyadenylation. The 3N nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the *tml* terminator, the nopaline synthase terminator, the pea rbcS E9 terminator, the terminator for the T7 transcript

from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3N end of the protease inhibitor I or II genes from potato or tomato, although other 3N elements known to those of skill in the art can also be employed. Alternatively, one also could use a gamma coixin, oleosin 3 or other terminator from the genus *Coix*.

5 Preferred 3' elements include those from the nopaline synthase gene of *Agrobacterium tumefaciens* (Bevan et al., 1983), the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato.

As the DNA sequence between the transcription initiation site and the start of the  
10 coding sequence, i.e., the untranslated leader sequence, can influence gene expression, one may also wish to employ a particular leader sequence. Preferred leader sequences are contemplated to include those which include sequences predicted to direct optimum expression of the attached gene, i.e., to include a preferred consensus leader sequence which may increase or maintain mRNA stability and prevent inappropriate initiation of translation. The choice of such  
15 sequences will be known to those of skill in the art in light of the present disclosure. Sequences that are derived from genes that are highly expressed in plants will be most preferred.

Other sequences that have been found to enhance gene expression in transgenic plants include intron sequences (e.g., from *Adh1*, *bronze1*, *actin1*, *actin 2* (WO 00/760067), or the  
20 sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other  
25 leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA  
30 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize

Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

Regulatory elements such as Adh intron 1 (Callis et al., 1987), sucrose synthase intron (Vasil et al., 1989) or TMV omega element (Gallie, et al., 1989), may further be included  
5 where desired.

Examples of enhancers include elements from the CaMV 35S promoter, octopine synthase genes (Ellis et al., 1987), the rice actin I gene, the maize alcohol dehydrogenase gene (Callis et al., 1987), the maize shrunken I gene (Vasil et al., 1989), TMV Omega element (Gallie et al., 1989) and promoters from non-plant eukaryotes (e.g. yeast; Ma et al., 1988).

10 Vectors for use in accordance with the present invention may be constructed to include the ocs enhancer element. This element was first identified as a 16 bp palindromic enhancer from the octopine synthase (ocs) gene of utilane (Ellis et al., 1987), and is present in at least 10 other promoters (Bouchez et al., 1989). The use of an enhancer element, such as the ocs element and particularly multiple copies of the element, will act to increase the level of  
15 transcription from adjacent promoters when applied in the context of monocot transformation.

Ultimately, the most desirable DNA segments for introduction into for example a monocot genome may be homologous genes or gene families which encode a desired trait (e.g., increased yield per acre) and which are introduced under the control of novel promoters or enhancers, etc., or perhaps even homologous or tissue specific (e.g., root-, collar/sheath-,  
20 whorl-, stalk-, earshank-, kernel- or leaf-specific) promoters or control elements. Indeed, it is envisioned that a particular use of the present invention will be the targeting of a gene in a constitutive manner or a root-specific manner. For example, insect resistant genes may be expressed specifically in the whorl and collar/sheath tissues which are targets for the first and second broods, respectively, of ECB. Likewise, genes encoding proteins with particular  
25 activity against rootworm may be targeted directly to root tissues.

Vectors for use in tissue-specific targeting of genes in transgenic plants will typically include tissue-specific promoters and may also include other tissue-specific control elements such as enhancer sequences. Promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These  
30 include, for example, the rbcS promoter, specific for green tissue; the ocs, nos and mas promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8)

35S promoter which directs enhanced expression in roots, an alpha-tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp ocs enhancer element from the octopine synthase (ocs) gene (Ellis et al., 1987; Bouchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Tissue specific expression may be functionally accomplished by introducing a constitutively expressed gene (all tissues) in combination with an antisense gene that is expressed only in those tissues where the gene product is not desired. For example, a gene coding for the crystal toxin protein from *B. thuringiensis* (Bt) may be introduced such that it is expressed in all tissues using the 35S promoter from Cauliflower Mosaic Virus. Expression of an antisense transcript of the Bt gene in a maize kernel, using for example a zein promoter, would prevent accumulation of the Bt protein in seed. Hence the protein encoded by the introduced gene would be present in all tissues except the kernel.

Expression of some genes in transgenic plants will be desired only under specified conditions. For example, it is proposed that expression of certain genes that confer resistance to environmental stress factors such as drought will be desired only under actual stress conditions. It is contemplated that expression of such genes throughout a plants development may have detrimental effects. It is known that a large number of genes exist that respond to the environment. For example, expression of some genes such as *rbcS*, encoding the small subunit of ribulose biphosphate carboxylase, is regulated by light as mediated through phytochrome. Other genes are induced by secondary stimuli. For example, synthesis of abscisic acid (ABA) is induced by certain environmental factors, including but not limited to water stress. A number of genes have been shown to be induced by ABA (Skriver and Mundy, 1990). It is also anticipated that expression of genes conferring resistance to insect predation would be desired only under conditions of actual insect infestation. Therefore, for some desired traits inducible expression of genes in transgenic plants will be desired.

Expression of a gene in a transgenic plant will be desired only in a certain time period during the development of the plant. Developmental timing is frequently correlated with tissue specific gene expression. For example, expression of zein storage proteins is initiated in the endosperm about 15 days after pollination.

Additionally, vectors may be constructed and employed in the intracellular targeting of a specific gene product within the cells of a transgenic plant or in directing a protein to the extracellular environment. This will generally be achieved by joining a DNA sequence encoding a transit or signal peptide sequence to the coding sequence of a particular gene. The resultant transit, or signal, peptide will transport the protein to a particular intracellular, or extracellular destination, respectively, and will then be post-translationally removed. Transit or signal peptides act by facilitating the transport of proteins through intracellular membranes, e.g., vacuole, vesicle, plastid and mitochondrial membranes, whereas signal peptides direct proteins through the extracellular membrane.

A particular example of such a use concerns the direction of a herbicide resistance gene, such as the EPSPS gene, to a particular organelle such as the chloroplast rather than to the cytoplasm. This is exemplified by the use of the rbcS transit peptide which confers plastid-specific targeting of proteins. In addition, it is proposed that it may be desirable to target certain genes responsible for male sterility to the mitochondria, or to target certain genes for resistance to phytopathogenic organisms to the extracellular spaces, or to target proteins to the vacuole.

By facilitating the transport of the protein into compartments inside and outside the cell, these sequences may increase the accumulation of gene product protecting them from proteolytic degradation. These sequences also allow for additional mRNA sequences from highly expressed genes to be attached to the coding sequence of the genes. Since mRNA being translated by ribosomes is more stable than naked mRNA, the presence of translatable mRNA in front of the gene may increase the overall stability of the mRNA transcript from the gene and thereby increase synthesis of the gene product. Since transit and signal sequences are usually post-translationally removed from the initial translation product, the use of these sequences allows for the addition of extra translated sequences that may not appear on the final polypeptide. Targeting of certain proteins may be desirable in order to enhance the stability of the protein (U.S. Patent No. 5,545,818).

It may be useful to target DNA itself within a cell. For example, it may be useful to target introduced DNA to the nucleus as this may increase the frequency of transformation. Within the nucleus itself it would be useful to target a gene in order to achieve site specific

integration. For example, it would be useful to have an gene introduced through transformation replace an existing gene in the cell.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific DNA sequence.

The invention relates to an isolated plant, e.g., *Arabidopsis* and rice, nucleic acid molecule, which directs the expression of linked nucleic acid fragment in a plant, e.g., in root or leaf or constitutively, as well as the corresponding open reading frame and encoded product. The nucleic acid molecule, e.g., one which comprises a promoter can be used to overexpress a linked nucleic acid fragment so as to express a product in a constitutive or tissue-specific manner, or to alter the expression of the product, e.g., via the use of antisense vectors or by "knocking out" the expression of at least one genomic copy of the gene.

Preferred sources from which the nucleic acid molecules of the invention can be obtained or isolated include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea utilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond



(*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, vegetables, ornamentals, and conifers.

Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa. Australina*, *Wa. Borealis*, *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa. Microscopica*, *Wa. Neglecta*) and genus *Wofieldia* (*Wl. utila*, *Wl. utilane* n, *Wl. gladiata*, *Wl. utila*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae – A Monograph Study. Geobotanisches Institut ETH, Stiftung Rubel, Zurich (1986)).

Vegetables from which to obtain or isolate the nucleic acid molecules of the invention include, but are not limited to, tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals from which to obtain or isolate the nucleic acid molecules of the invention include, but are not limited to, azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga utilane*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis*

*nootkatensis*). Leguminous plants from which the nucleic acid molecules of the invention can be isolated or obtained include, but are not limited to, beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, and the like. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo. Preferred forage and turf grass from which the nucleic acid molecules of the invention can be isolated or obtained for use in the methods of the invention include, but are not limited to, alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Other preferred sources of the nucleic acid molecules of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, utilan sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, utilane, and zucchini.

Yet other sources of nucleic acid molecules are ornamental plants including, but not limited to, impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, and plants such as those shown in Table 1.

25

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		<a href="http://www.cucurbit.org/">http://www.cucurbit.org/</a>
	<i>Cucumis melo</i>	Melon		<a href="http://genome.cornell.edu/cgc/">http://genome.cornell.edu/cgc/</a>
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash – winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				<a href="http://www.national.usda.gov/pgr/genetic/Map_proj/">http://www.national.usda.gov/pgr/genetic/Map_proj/</a>
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> <li>15x BAC on variety Heinz 1706 order from Clemson Genome center (<a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a>)</li> <li>11.6x BAC of <i>L. cheesmanii</i> (originates</li> </ul>	<a href="http://genome.cornell.edu/solgenes">genome.cornell.edu/solgenes</a> <a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/">http://ars-genome.cornell.edu/cgi-bin/WebAce/</a>

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES  RESOURCES	LINKS
			<p>from J. Giovannoni) available from Clemson genome center (<a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a>)</p> <ul style="list-style-type: none"> <li>• EST collection from TIGR (<a href="http://www.tigr.org/tdb/lgi/index.html">www.tigr.org/tdb/lgi/index.html</a>)</li> <li>• EST collection from Clemson Genome Center (<a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a>)</li> <li>• TAG 99:254-271, 1999 (esculentum x pennelli)</li> <li>• TAG 89:1007-1013, 1994 (peruvianum)</li> <li>• Plant Cell Reports 12:293-297, 1993 (RAPDs)</li> <li>• Genetics 132:1141-1160, 1992 (potato x tomato)</li> <li>• Genetics 120:1095-1105, 1988 (RFLP potato and tomato)</li> </ul>	<p><a href="#">webace?db=solgenes</a> <a href="http://genome.cornell.edu/tgc/">http://genome.cornell.edu/tgc/</a> <a href="http://tgrc.ucdavis.edu/">http://tgrc.ucdavis.edu/</a></p>

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
			<ul style="list-style-type: none"> <li>Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs)</li> </ul>	
	<i>Capsicum annuum</i>	Pepper		<a href="http://neptune.netimages.com/~chile/science.html">http://neptune.netimages.com/~chile/science.html</a>
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	( <i>Nicotiana tabacum</i> )	(Tobacco)		
	( <i>Solanum tuberosum</i> )	(Potato)		
	( <i>Petunia x hybrida hort. Ex E. Vilm.</i> )	(Petunia)	4x BAC of Petunia hybrida 7984 available from Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	
Total				<a href="http://www.nal.usda.gov/pgdic/Map_proj/">http://www.nal.usda.gov/pgdic/Map_proj/</a>
Brassicaceae	<i>Brassica</i>	Broccoli		<a href="http://res.agr">http://res.agr</a>

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES  RESOURCES	LINKS
	<i>oleracea</i> L. var. <i>italica</i>			<a href="http://ecorc.cwmt/crucifer/traits/index.htm">ca/ecorc/cwmt/crucifer/traits/index.htm</a> <a href="http://geneous.cit.cornell.edu/cabbage/aboutcab.html">http://geneous.cit.cornell.edu/cabbage/aboutcab.html</a>
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	( <i>Brassica napus</i> )	(Oilseed rape)		<a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb">http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb</a>
		Arabidopsis	12x and 6x BACs on Columbia strain available	<a href="http://ars-genome.cornell.edu">http://ars-genome.cornell.edu</a>

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES  RESOURCES	LINKS
			from Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	<a href="http://ll.edu/cgi-bin/WebAce/webace?db=agr">ll.edu/cgi-bin/WebAce/webace?db=agr</a>
Total				<a href="http://www.nal.usda.gov/pgdic/Map_proj/">http://www.nal.usda.gov/pgdic/Map_proj/</a>
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	( <i>Beta vulgaris</i> )	(Sugar Beet)		
Total				
Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	<a href="http://ars-genome.cornell.edu/cgi-">http://ars-genome.cornell.edu/cgi-</a>

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
				<a href="#">bin/WebAce/webace?db=beangenes</a>
	<i>Pisum sativum</i>	Pea		
	( <i>Glycine max</i> )	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	<a href="http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase">http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase</a>
Total			<a href="http://www.nal.usda.gov/pgdic/Map_proj/">http://www.nal.usda.gov/pgdic/Map_proj/</a>	
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center ( <a href="http://www.genome.clemson.edu">www.genome.clemson.edu</a> )	
	( <i>Zea mays</i> )	(Field Corn)		<a href="http://www.agron.missouri.edu/mnl/">http://www.agron.missouri.edu/mnl/</a>
Total			<a href="http://www.nal.usda.gov/pgdic/Map_proj/">http://www.nal.usda.gov/pgdic/Map_proj/</a>	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		



FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES  RESOURCES	LINKS
		(Garlic)		
		(Asparagus)		
Total			<a href="http://www.nal.usda.gov/pgd">http://www.nal.usda.gov/pgd</a> <a href="#">ic/Map_proj/</a>	

Preferred forage and turf grass nucleic acid sources for the nucleic acid molecules of the invention include, but are not limited to, alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Yet other preferred sources include, but are not limited to, crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, and the like), and even more preferably corn, rice and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence isolated or obtained from any plant which encodes a polypeptide having, e.g. at least 70% amino acid sequence identity to a polypeptide encoded by a gene comprising any one of SEQ ID NOs:1-339, 477-515, 517-526, 536-579, and 693-773, preferably any one of SEQ ID NOs: 536-579, more preferably of any one of SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter orthologs thereof, e.g., SEQ ID NOs:825-875, which include the minimal promoter region.. Based on the *Arabidopsis* nucleic acid sequence of the present invention, orthologs may be identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the *Arabidopsis* nucleic acid sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular *Arabidopsis* nucleic acid sequence is used as a probe that selectively hybridizes to other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from

any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g., Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from which the probe sequence is derived. The application of these methods using the *Arabidopsis* sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as  $^{32}\text{P}$ , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al. (1989). In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity or DNA having a specified nucleotide sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described herein.

For example, to identify orthologs of the sequences described herein, similarity searches are carried out in databases using a BLAST (see above) algorithm followed by analysis using SCAN (the Sequence Comparison Analysis, program version 1.0k licensed from the Los Alamos National Laboratories) software with added filters.

5        A rice database is searched (Table 14) as well as a database constructed from GenBank (Table 15). Using a PERL script, a subset of the GenBank database (GenBank version 123.0). The database contains all of the plant translated regions from GenBank, with the exception of *Arabidopsis thaliana* sequences. In addition, the GenBank subset database retains annotation from following fields: product, function, note, as well as protein and nucleotide accession  
10        numbers and organisms.  
The BLASTX search algorithm, which translates a query sequence in all six frames and then carries out a protein comparison, is selected to conduct the search. Queries are executed using the "blastall" command with the following parameters: "-p blastp", "-v 50", "-b 50", "-F F". Homologies to hypothetical sequences are eliminated by setting the default parameters  
15        of SCAN at the command line to "-a 60 60" (60 identities and 60 percent identity, i.e., such that all of the results have 60 or more identities and that 60% of the alignment is made up of identities). In addition to SCAN, a E-value cutoff of  $\leq 1e-4$  is implemented.

It is specifically contemplated by the inventors that one could mutagenize a promoter to, for example, potentially improve the utility of the elements for the expression of transgenes in  
20        plants. The mutagenesis of these elements can be carried out at random and the mutagenized promoter sequences screened for activity in a trial-by-error procedure.

Alternatively, particular sequences which provide the promoter with desirable expression characteristics, or the promoter with expression enhancement activity, could be identified and these or similar sequences introduced into the sequences via mutation. It is  
25        further contemplated that one could mutagenize these sequences in order to enhance their expression of transgenes in a particular species.

The means for mutagenizing a DNA segment encoding a promoter sequence of the current invention are well-known to those of skill in the art. As indicated, modifications to promoter or other regulatory element may be made by random, or site-specific mutagenesis  
30        procedures. The promoter and other regulatory element may be modified by altering their

structure through the addition or deletion of one or more nucleotides from the sequence which encodes the corresponding un-modified sequences.

Mutagenesis may be performed in accordance with any of the techniques known in the art, such as, and not limited to, synthesizing an oligonucleotide having one or more mutations within the sequence of a particular regulatory region. In particular, site-specific mutagenesis is a technique useful in the preparation of promoter mutants, through specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to about 75 nucleotides or more in length is preferred, with about 10 to about 25 or more residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art, as exemplified by various publications. As will be appreciated, the technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially available and their use is generally well known to those skilled in the art.

Double stranded plasmids also are routinely employed in site directed mutagenesis which eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double stranded vector which includes within its sequence a DNA sequence which encodes the promoter. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation.

This heteroduplex vector is then used to transform or transfect appropriate cells, such as *E. coli* cells, and cells are selected which include recombinant vectors bearing the mutated sequence arrangement. Vector DNA can then be isolated from these cells and used for plant transformation. A genetic selection scheme was devised by Kunkel et al. (1987) to enrich for clones incorporating mutagenic oligonucleotides. Alternatively, the use of PCR with commercially available thermostable enzymes such as Taq polymerase may be used to incorporate a mutagenic oligonucleotide primer into an amplified DNA fragment that can then be cloned into an appropriate cloning or expression vector. The PCR-mediated mutagenesis procedures of Tomic et al. (1990) and Upender et al. (1995) provide two examples of such protocols. A PCR employing a thermostable ligase in addition to a thermostable polymerase also may be used to incorporate a phosphorylated mutagenic oligonucleotide into an amplified DNA fragment that may then be cloned into an appropriate cloning or expression vector. The mutagenesis procedure described by Michael (1994) provides an example of one such protocol.

The preparation of sequence variants of the selected promoter-encoding DNA segments using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of DNA sequences may be obtained. For example, recombinant vectors encoding the desired promoter sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

In addition, an unmodified or modified nucleotide sequence of the present invention can be varied by shuffling the sequence of the invention. To test for a function of variant DNA sequences according to the invention, the sequence of interest is operably linked to a selectable or screenable marker gene and expression of the marker gene is tested in transient expression assays with protoplasts or in stably transformed plants. It is known to the skilled artisan that DNA sequences capable of driving expression of an associated nucleotide sequence are built in a modular way. Accordingly, expression levels from shorter DNA fragments may be different than the one from the longest fragment and may be different from each other. For example, deletion of a down-regulating upstream element will lead to an increase in the expression levels of the associated nucleotide sequence while deletion of an up-regulating element will decrease the expression levels of the associated nucleotide sequence. It is also known to the skilled

artisan that deletion of development-specific or a tissue-specific element will lead to a temporally or spatially altered expression profile of the associated nucleotide sequence.

Embraced by the present invention are also functional equivalents of the promoters of the present invention, i.e. nucleotide sequences that hybridize under stringent conditions to any one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, or 693-773, preferably to any one of  
5 SEQ ID NOs: 536-579, more preferably to any one of SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter orthologs thereof. As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the  
10 concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" also is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template-dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the  
15 sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson and Rarnstad, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U.S. Patent No. 4,237,224. A  
20 number of template dependent processes are available to amplify the target sequences of interest present in a sample, such methods being well known in the art and specifically disclosed herein below.

Where a clone comprising a promoter has been isolated in accordance with the instant invention, one may wish to delimit the essential promoter regions within the clone. One  
25 efficient, targeted means for preparing mutagenizing promoters relies upon the identification of putative regulatory elements within the promoter sequence. This can be initiated by comparison with promoter sequences known to be expressed in similar tissue-specific or developmentally unique manner. Sequences which are shared among promoters with similar expression patterns are likely candidates for the binding of transcription factors and are thus  
30 likely elements which confer expression patterns. Confirmation of these putative regulatory elements can be achieved by deletion analysis of each putative regulatory region followed by

functional analysis of each deletion construct by assay of a reporter gene which is functionally attached to each construct. As such, once a starting promoter sequence is provided, any of a number of different deletion mutants of the starting promoter could be readily prepared.

As indicated above, deletion mutants, deletion mutants of the promoter of the invention  
5 also could be randomly prepared and then assayed. With this strategy, a series of constructs are prepared, each containing a different portion of the clone (a subclone), and these constructs are then screened for activity. A suitable means for screening for activity is to attach a deleted promoter or intron construct which contains a deleted segment to a selectable or screenable marker, and to isolate only those cells expressing the marker gene. In this way, a number of  
10 different, deleted promoter constructs are identified which still retain the desired, or even enhanced, activity. The smallest segment which is required for activity is thereby identified through comparison of the selected constructs. This segment may then be used for the construction of vectors for the expression of exogenous genes.

In order to improve the ability to identify transformants, one may desire to employ a  
15 selectable or screenable marker gene as, or in addition to, the expressible gene of interest. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can `select` for by chemical means, i.e., through  
20 the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait, the green fluorescent protein (GFP)). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which  
25 encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in  
30 extracellular solution (e.g., alpha-amylase, beta-lactamase, phosphinothricin acetyltransferase);

and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a protein that becomes sequestered in the cell wall, and which protein includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

One example of a protein suitable for modification in this manner is extensin, or hydroxyproline rich glycoprotein (HPRG). For example, the maize HPRG (Steifel et al., 1990) molecule is well characterized in terms of molecular biology, expression and protein structure. However, any one of a variety of utilane and/or glycine-rich wall proteins (Keller et al., 1989) could be modified by the addition of an antigenic site to create a screenable marker.

One exemplary embodiment of a secretable screenable marker concerns the use of a maize sequence encoding the wall protein HPRG, modified to include a 15 residue epitope from the pro-region of murine interleukin, however, virtually any detectable epitope may be employed in such embodiments, as selected from the extremely wide variety of antigen-antibody combinations known to those of skill in the art. The unique extracellular epitope can then be straightforwardly detected using antibody labeling in conjunction with chromogenic or fluorescent adjuncts.

Elements of the present disclosure may be exemplified in detail through the use of the bar and/or GUS genes, and also through the use of various other markers. Of course, in light of this disclosure, numerous other possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth hereinbelow. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant.



Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene (Potrykus et al., 1985) which codes for kanamycin resistance and can be selected for using kanamycin, G418, paromomycin, and the like; a *bar* gene which codes for bialaphos or phosphinothricin resistance; a gene which encodes an altered EPSP synthase protein (Hinchey et al., 1988) thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil (Stalker et al., 1988); a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonylurea or other ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene (Thillet et al., 1988); a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Preferred selectable marker genes encode phosphinothricin acetyltransferase; glyphosate resistant EPSPS, aminoglycoside phosphotransferase; hygromycin phosphotransferase, or neomycin phosphotransferase. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a suitable chloroplast transit peptide, CTP (European Patent Application 0,218,571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces hygroscopicus* or the *pat* gene from *Streptomyces viridochromogenes*. The enzyme phosphinothricin acetyl transferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, (Murakami et al., 1986; Twell et al., 1989) causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals (Potrykus, 1989).

Where one desires to employ a bialaphos resistance gene in the practice of the invention, a particularly useful gene for this purpose is the *bar* or *pat* genes obtainable from species of *Streptomyces* (e.g., ATCC No. 21,705). The cloning of the *bar* gene has been described (Murakami et al., 1986; Thompson et al., 1987) as has the use of the *bar* gene in the context of plants other than monocots (De Block et al., 1987; De Block et al., 1989).

Selection markers resulting in positive selection, such as a phosphomannose isomerase gene, as described in patent application WO 93/05163, may also be used. Alternative genes to

be used for positive selection are described in WO 94/20627 and encode xyloisomerases and phosphomanno-isomerases such as mannose-6-phosphate isomerase and mannose-1-phosphate isomerase; phosphomanno mutase; mannose epimerases such as those which convert carbohydrates to mannose or mannose to carbohydrates such as glucose or galactose; phosphatases such as mannose or xylose phosphatase, mannose-6-phosphatase and mannose-1-phosphatase, and permeases which are involved in the transport of mannose, or a derivative, or a precursor thereof into the cell. Transformed cells are identified without damaging or killing the non-transformed cells in the population and without co-introduction of antibiotic or herbicide resistance genes. As described in WO 93/05163, in addition to the fact that the need for antibiotic or herbicide resistance genes is eliminated, it has been shown that the positive selection method is often far more efficient than traditional negative selection.

Screenable markers that may be employed include, but are not limited to, a beta-glucuronidase (GUS) or *uidA* gene which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta et al., 1988); a beta-lactamase gene (Sutcliffe, 1978), which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xylE* gene (Zukowsky et al., 1983) which encodes a catechol dioxygenase that can convert chromogenic catechols; an  $\alpha$ -amylase gene (Ikuta et al., 1990); a tyrosinase gene (Katz et al., 1983) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a  $\beta$ -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene (Ow et al., 1986), which allows for bioluminescence detection; or even an aequorin gene (Prasher et al., 1985), which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein gene (Niedz et al., 1995).

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will

transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22 which contains the *rg*-Stadler allele and TR112, a K55 derivative which is *r-g, b, P1*. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

It is further proposed that R gene regulatory regions may be employed in chimeric constructs in order to provide mechanisms for controlling the expression of chimeric genes. More diversity of phenotypic expression is known at the R locus than at any other locus (Coe et al., 1988). It is contemplated that regulatory regions obtained from regions 5' to the structural R gene would be valuable in directing the expression of genes, e.g., insect resistance, drought resistance, herbicide tolerance or other protein coding regions. For the purposes of the present invention, it is believed that any of the various R gene family members may be successfully employed (e.g., P, S, Lc, etc.). However, the most preferred will generally be Sn (particularly Sn:bol3). Sn is a dominant member of the R gene complex and is functionally similar to the R and B loci in that Sn controls the tissue specific deposition of anthocyanin pigments in certain seedling and plant cells, therefore, its phenotype is similar to R.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening. Where use of a screenable marker gene such as *lux* or GFP is desired, benefit may be realized by creating a gene fusion between the screenable marker gene and a selectable marker gene, for example, a GFP-NPTII gene fusion. This could allow, for example, selection of transformed cells followed by screening of transgenic plants or seeds.

Genes of interest are reflective of the commercial markets and interests of those involved in the development of the crop. Crops and markets of interest changes, and as

developing nations open up world markets, new crops and technologies will also emerge. In addition, as the understanding of agronomic traits and characteristics such as yield and heterosis increase, the choice of genes for transformation will change accordingly. General categories of genes of interest include, for example, those genes involved in information, such as zinc fingers, those involved in communication, such as kinases, and those involved in housekeeping, such as heat shock proteins. More specific categories of transgenes, for example, include genes encoding important traits for agronomics, insect resistance, disease resistance, herbicide resistance, sterility, grain characteristics, and commercial products. Genes of interest include, generally, those involved in starch, oil, carbohydrate, or nutrient metabolism, as well as those affecting kernel size, sucrose loading, zinc finger proteins, see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311, and the like.

One skilled in the art recognizes that the expression level and regulation of a transgene in a plant can vary significantly from line to line. Thus, one has to test several lines to find one with the desired expression level and regulation. Once a line is identified with the desired regulation specificity of a chimeric Cre transgene, it can be crossed with lines carrying different inactive replicons or inactive transgene for activation.

Other sequences which may be linked to the gene of interest which encodes a polypeptide are those which can target to a specific organelle, e.g., to the mitochondria, nucleus, or plastid, within the plant cell. Targeting can be achieved by providing the polypeptide with an appropriate targeting peptide sequence, such as a secretory signal peptide (for secretion or cell wall or membrane targeting, a plastid transit peptide, a chloroplast transit peptide, e.g., the chlorophyll a/b binding protein, a mitochondrial target peptide, a vacuole targeting peptide, or a nuclear targeting peptide, and the like. For example, the small subunit of ribulose biphosphate carboxylase transit peptide, the EPSPS transit peptide or the dihydrodipicolinic acid synthase transit peptide may be used. For examples of plastid organelle targeting sequences (see WO 00/12732). Plastids are a class of plant organelles derived from proplastids and include chloroplasts, leucoplasts, aravloplast, and chromoplasts. The plastids are major sites of biosynthesis in plants. In addition to photosynthesis in the chloroplast, plastids are also sites of lipid biosynthesis, nitrate reduction to ammonium, and starch storage. And while plastids contain their own circular genome, most of the proteins localized to the

plastids are encoded by the nuclear genome and are imported into the organelle from the cytoplasm.

Transgenes used with the present invention will often be genes that direct the expression of a particular protein or polypeptide product, but they may also be non-expressible DNA segments, e.g., transposons such as Ds that do not direct their own transposition. As used herein, an "expressible gene" is any gene that is capable of being transcribed into RNA (e.g., mRNA, antisense RNA, etc.) or translated into a protein, expressed as a trait of interest, or the like, etc., and is not limited to selectable, screenable or non-selectable marker genes. The invention also contemplates that, where both an expressible gene that is not necessarily a marker gene is employed in combination with a marker gene, one may employ the separate genes on either the same or different DNA segments for transformation. In the latter case, the different vectors are delivered concurrently to recipient cells to maximize cotransformation.

The choice of the particular DNA segments to be delivered to the recipient cells will often depend on the purpose of the transformation. One of the major purposes of transformation of crop plants is to add some commercially desirable, agronomically important traits to the plant. Such traits include, but are not limited to, herbicide resistance or tolerance; insect resistance or tolerance; disease resistance or tolerance (viral, bacterial, fungal, nematode); stress tolerance and/or resistance, as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress; oxidative stress; increased yields; food content and makeup; physical appearance; male sterility; drydown; standability; prolificacy; starch properties; oil quantity and quality; and the like. One may desire to incorporate one or more genes conferring any such desirable trait or traits, such as, for example, a gene or genes encoding pathogen resistance.

In certain embodiments, the present invention contemplates the transformation of a recipient cell with more than one advantageous transgene. Two or more transgenes can be supplied in a single transformation event using either distinct transgene-encoding vectors, or using a single vector incorporating two or more gene coding sequences. For example, plasmids bearing the *bar* and *aroA* expression units in either convergent, divergent, or colinear orientation, are considered to be particularly useful. Further preferred combinations are those of an insect resistance gene, such as a *Bt* gene, along with a protease inhibitor gene such as *pinII*, or the use of *bar* in combination with either of the above genes. Of course, any two or

more transgenes of any description, such as those conferring herbicide, insect, disease (viral, bacterial, fungal, nematode) or drought resistance, male sterility, drydown, standability, prolificacy, starch properties, oil quantity and quality, or those increasing yield or nutritional quality may be employed as desired.

5           The genes encoding phosphinothricin acetyltransferase (*bar* and *pat*), glyphosate tolerant EPSP synthase genes, the glyphosate degradative enzyme gene *gox* encoding glyphosate oxidoreductase, *deh* (encoding a dehalogenase enzyme that inactivates dalapon), herbicide resistant (e.g., sulfonyleurea and imidazolinone) acetolactate synthase, and *bxn* genes (encoding a nitrilase enzyme that degrades bromoxynil) are good examples of herbicide  
10       resistant genes for use in transformation. The *bar* and *pat* genes code for an enzyme, phosphinothricin acetyltransferase (PAT), which inactivates the herbicide phosphinothricin and prevents this compound from inhibiting glutamine synthetase enzymes. The enzyme 5-enolpyruvylshikimate 3-phosphate synthase (EPSP Synthase), is normally inhibited by the herbicide N-(phosphonomethyl)glycine (glyphosate). However, genes are known that encode  
15       glyphosate-resistant EPSP Synthase enzymes.

          These genes are particularly contemplated for use in monocot transformation. The *deh* gene encodes the enzyme dalapon dehalogenase and confers resistance to the herbicide dalapon. The *bxn* gene codes for a specific nitrilase enzyme that converts bromoxynil to a non-herbicidal degradation product.

20           An important aspect of the present invention concerns the introduction of insect resistance-conferring genes into plants. Potential insect resistance genes which can be introduced include *Bacillus thuringiensis* crystal toxin genes or *Bt* genes (Watrud et al., 1985). *Bt* genes may provide resistance to lepidopteran or coleopteran pests such as European Corn Borer (ECB) and corn rootworm (CRW). Preferred *Bt* toxin genes for use in such  
25       embodiments include the CryIA(b) and CryIA(c) genes. Endotoxin genes from other species of *B. thuringiensis* which affect insect growth or development may also be employed in this regard.

          The poor expression of *Bt* toxin genes in plants is a well-documented phenomenon, and the use of different promoters, fusion proteins, and leader sequences has not led to significant  
30       increases in *Bt* protein expression (Vaeck et al., 1989; Barton et al., 1987). It is therefore contemplated that the most advantageous *Bt* genes for use in the transformation protocols

disclosed herein will be those in which the coding sequence has been modified to effect increased expression in plants, and more particularly, those in which maize preferred codons have been used. Examples of such modified *Bt* toxin genes include the variant *Bt* CryIA(b) gene termed Iab6 (Perlak et al., 1991) and the synthetic CryIA(c) genes termed 1800a and 1800b.

Protease inhibitors may also provide insect resistance (Johnson et al., 1989), and will thus have utility in plant transformation. The use of a protease inhibitor II gene, *pinII*, from tomato or potato is envisioned to be particularly useful. Even more advantageous is the use of a *pinII* gene in combination with a *Bt* toxin gene, the combined effect of which has been discovered by the present inventors to produce synergistic insecticidal activity. Other genes which encode inhibitors of the insects' digestive system, or those that encode enzymes or co-factors that facilitate the production of inhibitors, may also be useful. This group may be exemplified by oryzacystatin and amylase inhibitors, such as those from wheat and barley.

Also, genes encoding lectins may confer additional or alternative insecticide properties. Lectins (originally termed phytohemagglutinins) are multivalent carbohydrate-binding proteins which have the ability to agglutinate red blood cells from a range of species. Lectins have been identified recently as insecticidal agents with activity against weevils, ECB and rootworm (Murdock et al., 1990; Czapla and Lang, 1990). Lectin genes contemplated to be useful include, for example, barley and wheat germ agglutinin (WGA) and rice lectins (Gatehouse et al., 1984), with WGA being preferred.

Genes controlling the production of large or small polypeptides active against insects when introduced into the insect pests, such as, e.g., lytic peptides, peptide hormones and toxins and venoms, form another aspect of the invention. For example, it is contemplated that the expression of juvenile hormone esterase, directed towards specific insect pests, may also result in insecticidal activity, or perhaps cause cessation of metamorphosis (Hammock et al., 1990).

Transgenic plants expressing genes which encode enzymes that affect the integrity of the insect cuticle form yet another aspect of the invention. Such genes include those encoding, e.g., chitinase, proteases, lipases and also genes for the production of nikkomycin, a compound that inhibits chitin synthesis, the introduction of any of which is contemplated to produce insect resistant maize plants. Genes that code for activities that affect insect molting, such those

affecting the production of ecdysteroid UDP-glucosyl transferase, also fall within the scope of the useful transgenes of the present invention.

Genes that code for enzymes that facilitate the production of compounds that reduce the nutritional quality of the host plant to insect pests are also encompassed by the present invention. It may be possible, for instance, to confer insecticidal activity on a plant by altering its sterol composition. Sterols are obtained by insects from their diet and are used for hormone synthesis and membrane stability. Therefore alterations in plant sterol composition by expression of novel genes, e.g., those that directly promote the production of undesirable sterols or those that convert desirable sterols into undesirable forms, could have a negative effect on insect growth and/or development and hence endow the plant with insecticidal activity. Lipoxigenases are naturally occurring plant enzymes that have been shown to exhibit anti-nutritional effects on insects and to reduce the nutritional quality of their diet. Therefore, further embodiments of the invention concern transgenic plants with enhanced lipoxigenase activity which may be resistant to insect feeding.

The present invention also provides methods and compositions by which to achieve qualitative or quantitative changes in plant secondary metabolites. One example concerns transforming plants to produce DIMBOA which, it is contemplated, will confer resistance to European corn borer, rootworm and several other maize insect pests. Candidate genes that are particularly considered for use in this regard include those genes at the *bx* locus known to be involved in the synthetic DIMBOA pathway (Dunn et al., 1981). The introduction of genes that can regulate the production of maysin, and genes involved in the production of dhurrin in sorghum, is also contemplated to be of use in facilitating resistance to earworm and rootworm, respectively.

*Tripsacum dactyloides* is a species of grass that is resistant to certain insects, including corn root worm. It is anticipated that genes encoding proteins that are toxic to insects or are involved in the biosynthesis of compounds toxic to insects will be isolated from *Tripsacum* and that these novel genes will be useful in conferring resistance to insects. It is known that the basis of insect resistance in *Tripsacum* is genetic, because said resistance has been transferred to *Zea mays* via sexual crosses (Branson and Guss, 1972).

Further genes encoding proteins characterized as having potential insecticidal activity may also be used as transgenes in accordance herewith. Such genes include, for example, the



cowpea trypsin inhibitor (CpTI; Hilder et al., 1987) which may be used as a rootworm deterrent; genes encoding avermectin (Campbell, 1989; Ikeda et al., 1987) which may prove particularly useful as a corn rootworm deterrent; ribosome inactivating protein genes; and even genes that regulate plant structures. Transgenic maize including anti-insect antibody genes and genes that code for enzymes that can covert a non-toxic insecticide (pro-insecticide) applied to the outside of the plant into an insecticide inside the plant are also contemplated.

Improvement of a plant's ability to tolerate various environmental stresses such as, but not limited to, drought, excess moisture, chilling, freezing, high temperature, salt, and oxidative stress, can also be effected through expression of heterologous, or overexpression of homologous genes. Benefits may be realized in terms of increased resistance to freezing temperatures through the introduction of an "antifreeze" protein such as that of the Winter Flounder (Cutler et al., 1989) or synthetic gene derivatives thereof. Improved chilling tolerance may also be conferred through increased expression of glycerol-3-phosphate acetyltransferase in chloroplasts (Murata et al., 1992; Wolter et al., 1992). Resistance to oxidative stress (often exacerbated by conditions such as chilling temperatures in combination with high light intensities) can be conferred by expression of superoxide dismutase (Gupta et al., 1993), and may be improved by glutathione reductase (Bowler et al., 1992). Such strategies may allow for tolerance to freezing in newly emerged fields as well as extending later maturity higher yielding varieties to earlier relative maturity zones.

Expression of novel genes that favorably effect plant water content, total water potential, osmotic potential, and turgor can enhance the ability of the plant to tolerate drought. As used herein, the terms "drought resistance" and "drought tolerance" are used to refer to a plants increased resistance or tolerance to stress induced by a reduction in water availability, as compared to normal circumstances, and the ability of the plant to function and survive in lower-water environments, and perform in a relatively superior manner. In this aspect of the invention it is proposed, for example, that the expression of a gene encoding the biosynthesis of osmotically-active solutes can impart protection against drought. Within this class of genes are DNAs encoding mannitol dehydrogenase (Lee and Saier, 1982) and trehalose-6-phosphate synthase (Kaasen et al., 1992). Through the subsequent action of native phosphatases in the cell or by the introduction and coexpression of a specific phosphatase, these introduced genes will result in the accumulation of either mannitol or trehalose, respectively, both of which have

been well documented as protective compounds able to mitigate the effects of stress. Mannitol accumulation in transgenic tobacco has been verified and preliminary results indicate that plants expressing high levels of this metabolite are able to tolerate an applied osmotic stress (Tarczynski et al., cited supra (1992), 1993).

5 Similarly, the efficacy of other metabolites in protecting either enzyme function (e.g. alanopine or propionic acid) or membrane integrity (e.g., alanopine) has been documented (Loomis et al., 1989), and therefore expression of gene encoding the biosynthesis of these compounds can confer drought resistance in a manner similar to or complimentary to mannitol. Other examples of naturally occurring metabolites that are osmotically active and/or provide  
10 some direct protective effect during drought and/or desiccation include sugars and sugar derivatives such as fructose, erythritol (Coxson et al., 1992), sorbitol, dulcitol (Karsten et al., 1992), glucosylglycerol (Reed et al., 1984; Erdmann et al., 1992), sucrose, stachyose (Koster and Leopold, 1988; Blackman et al., 1992), ononitol and pinitol (Vernon and Bohnert, 1992), and raffinose (Bernal-Lugo and Leopold, 1992). Other osmotically active solutes which are  
15 not sugars include, but are not limited to, proline and glycine-betaine (Wyn-Jones and Storey, 1981). Continued canopy growth and increased reproductive fitness during times of stress can be augmented by introduction and expression of genes such as those controlling the osmotically active compounds discussed above and other such compounds, as represented in one exemplary embodiment by the enzyme myoinositol 0-methyltransferase.

20 It is contemplated that the expression of specific proteins may also increase drought tolerance. Three classes of Late Embryogenic Proteins have been assigned based on structural similarities (see Dure et al., 1989). All three classes of these proteins have been demonstrated in maturing (i.e., desiccating) seeds. Within these 3 types of proteins, the Type-II (dehydrin-type) have generally been implicated in drought and/or desiccation tolerance in vegetative plant  
25 parts (i.e. Mundy and Chua, 1988; Piatkowski et al., 1990; Yamaguchi-Shinozaki et al., 1992). Recently, expression of a Type-III LEA (HVA-1) in tobacco was found to influence plant height, maturity and drought tolerance (Fitzpatrick, 1993). Expression of structural genes from all three groups may therefore confer drought tolerance. Other types of proteins induced during water stress include thiol proteases, aldolases and transmembrane transporters  
30 (Guerrero et al., 1990), which may confer various protective and/or repair-type functions

during drought stress. The expression of a gene that effects lipid biosynthesis and hence membrane composition can also be useful in conferring drought resistance on the plant.

Many genes that improve drought resistance have complementary modes of action. Thus, combinations of these genes might have additive and/or synergistic effects in improving drought resistance in plants. Many of these genes also improve freezing tolerance (or resistance); the physical stresses incurred during freezing and drought are similar in nature and may be mitigated in similar fashion. Benefit may be conferred via constitutive expression of these genes, but the preferred means of expressing these novel genes may be through the use of a turgor-induced promoter (such as the promoters for the turgor-induced genes described in Guerrero et al. 1990 and Shagan et al., 1993). Spatial and temporal expression patterns of these genes may enable maize to better withstand stress.

Expression of genes that are involved with specific morphological traits that allow for increased water extractions from drying soil would be of benefit. For example, introduction and expression of genes that alter root characteristics may enhance water uptake. Expression of genes that enhance reproductive fitness during times of stress would be of significant value. For example, expression of DNAs that improve the synchrony of pollen shed and receptiveness of the female flower parts, i.e., silks, would be of benefit. In addition, expression of genes that minimize kernel abortion during times of stress would increase the amount of grain to be harvested and hence be of value. Regulation of cytokinin levels in monocots, such as maize, by introduction and expression of an isopentenyl transferase gene with appropriate regulatory sequences can improve monocot stress resistance and yield (Gan et al., Science, 270:1986 (1995)).

Given the overall role of water in determining yield, it is contemplated that enabling plants to utilize water more efficiently, through the introduction and expression of novel genes, will improve overall performance even when soil water availability is not limiting. By introducing genes that improve the ability of plants to maximize water usage across a full range of stresses relating to water availability, yield stability or consistency of yield performance may be realized.

It is proposed that increased resistance to diseases may be realized through introduction of genes into plants period. It is possible to produce resistance to diseases caused by viruses, bacteria, fungi, root pathogens, insects and nematodes. It is also contemplated that

control of mycotoxin producing organisms may be realized through expression of introduced genes.

Resistance to viruses may be produced through expression of novel genes. For example, it has been demonstrated that expression of a viral coat protein in a transgenic plant can impart resistance to infection of the plant by that virus and perhaps other closely related viruses (Cuozzo et al., 1988, Hemenway et al., 1988, Abel et al., 1986). It is contemplated that expression of antisense genes targeted at essential viral functions may impart resistance to said virus. For example, an antisense gene targeted at the gene responsible for replication of viral nucleic acid may inhibit said replication and lead to resistance to the virus. It is believed that interference with other viral functions through the use of antisense genes may also increase resistance to viruses. Further it is proposed that it may be possible to achieve resistance to viruses through other approaches, including, but not limited to the use of satellite viruses.

It is proposed that increased resistance to diseases caused by bacteria and fungi may be realized through introduction of novel genes. It is contemplated that genes encoding so-called "peptide antibiotics," pathogenesis related (PR) proteins, toxin resistance, and proteins affecting host-pathogen interactions such as morphological characteristics will be useful. Peptide antibiotics are polypeptide sequences which are inhibitory to growth of bacteria and other microorganisms. For example, the classes of peptides referred to as cecropins and magainins inhibit growth of many species of bacteria and fungi. It is proposed that expression of PR proteins in plants may be useful in conferring resistance to bacterial disease. These genes are induced following pathogen attack on a host plant and have been divided into at least five classes of proteins (Bol et al., 1990). Included amongst the PR proteins are beta-1,3-glucanases, chitinases, and osmotin and other proteins that are believed to function in plant resistance to disease organisms. Other genes have been identified that have antifungal properties, e.g., UDA (stinging nettle lectin) and hevein (Broakgert et al., 1989; Barkai-Golan et al., 1978). It is known that certain plant diseases are caused by the production of phytotoxins. Resistance to these diseases could be achieved through expression of a novel gene that encodes an enzyme capable of degrading or otherwise inactivating the phytotoxin. Expression novel genes that alter the interactions between the host plant and pathogen may be useful in reducing the ability the disease organism to invade the tissues of the host plant, e.g., an increase in the waxiness of the leaf cuticle or other morphological characteristics.

Plant parasitic nematodes are a cause of disease in many plants. It is proposed that it would be possible to make the plant resistant to these organisms through the expression of novel genes. It is anticipated that control of nematode infestations would be accomplished by altering the ability of the nematode to recognize or attach to a host plant and/or enabling the  
5 plant to produce nematicidal compounds, including but not limited to proteins.

Production of mycotoxins, including aflatoxin and fumonisin, by fungi associated with plants is a significant factor in rendering the grain not useful. These fungal organisms do not cause disease symptoms and/or interfere with the growth of the plant, but they produce chemicals (mycotoxins) that are toxic to animals. Inhibition of the growth of these fungi would  
10 reduce the synthesis of these toxic substances and, therefore, reduce grain losses due to mycotoxin contamination. Novel genes may be introduced into plants that would inhibit synthesis of the mycotoxin without interfering with fungal growth. Expression of a novel gene which encodes an enzyme capable of rendering the mycotoxin nontoxic would be useful in order to achieve reduced mycotoxin contamination of grain. The result of any of the above  
15 mechanisms would be a reduced presence of mycotoxins on grain.

Genes may be introduced into plants, particularly commercially important cereals such as maize, wheat or rice, to improve the grain for which the cereal is primarily grown. A wide range of novel transgenic plants produced in this manner may be envisioned depending on the particular end use of the grain.

For example, the largest use of maize grain is for feed or food. Introduction of genes  
20 that alter the composition of the grain may greatly enhance the feed or food value. The primary components of maize grain are starch, protein, and oil. Each of these primary components of maize grain may be improved by altering its level or composition. Several examples may be mentioned for illustrative purposes but in no way provide an exhaustive list  
25 of possibilities.

The protein of many cereal grains is suboptimal for feed and food purposes especially when fed to pigs, poultry, and humans. The protein is deficient in several amino acids that are essential in the diet of these species, requiring the addition of supplements to the grain. Limiting essential amino acids may include lysine, methionine, tryptophan, threonine, valine,  
30 arginine, and histidine. Some amino acids become limiting only after the grain is supplemented with other inputs for feed formulations. For example, when the grain is supplemented with

soybean meal to meet lysine requirements, methionine becomes limiting. The levels of these essential amino acids in seeds and grain may be elevated by mechanisms which include, but are not limited to, the introduction of genes to increase the biosynthesis of the amino acids, decrease the degradation of the amino acids, increase the storage of the amino acids in proteins, or increase transport of the amino acids to the seeds or grain.

One mechanism for increasing the biosynthesis of the amino acids is to introduce genes that deregulate the amino acid biosynthetic pathways such that the plant can no longer adequately control the levels that are produced. This may be done by deregulating or bypassing steps in the amino acid biosynthetic pathway which are normally regulated by levels of the amino acid end product of the pathway. Examples include the introduction of genes that encode deregulated versions of the enzymes aspartokinase or dihydrodipicolinic acid (DHDP)-synthase for increasing lysine and threonine production, and anthranilate synthase for increasing tryptophan production. Reduction of the catabolism of the amino acids may be accomplished by introduction of DNA sequences that reduce or eliminate the expression of genes encoding enzymes that catalyse steps in the catabolic pathways such as the enzyme lysine-ketoglutarate reductase.

The protein composition of the grain may be altered to improve the balance of amino acids in a variety of ways including elevating expression of native proteins, decreasing expression of those with poor composition, changing the composition of native proteins, or introducing genes encoding entirely new proteins possessing superior composition. DNA may be introduced that decreases the expression of members of the zein family of storage proteins. This DNA may encode ribozymes or antisense sequences directed to impairing expression of zein proteins or expression of regulators of zein expression such as the opaque-2 gene product. The protein composition of the grain may be modified through the phenomenon of cosuppression, i.e., inhibition of expression of an endogenous gene through the expression of an identical structural gene or gene fragment introduced through transformation (Goring et al., 1991). Additionally, the introduced DNA may encode enzymes which degrade seines. The decreases in zein expression that are achieved may be accompanied by increases in proteins with more desirable amino acid composition or increases in other major seed constituents such as starch. Alternatively, a chimeric gene may be introduced that comprises a coding sequence for a native protein of adequate amino acid composition such as for one of the globulin

proteins or 10 kD zein of maize and a promoter or other regulatory sequence designed to elevate expression of said protein. The coding sequence of said gene may include additional or replacement codons for essential amino acids. Further, a coding sequence obtained from another species, or, a partially or completely synthetic sequence encoding a completely unique peptide sequence designed to enhance the amino acid composition of the seed may be employed.

The introduction of genes that alter the oil content of the grain may be of value. Increases in oil content may result in increases in metabolizable energy content and density of the seeds for uses in feed and food. The introduced genes may encode enzymes that remove or reduce rate-limitations or regulated steps in fatty acid or lipid biosynthesis. Such genes may include, but are not limited to, those that encode acetyl-CoA carboxylase, ACP-acyltransferase, beta-ketoacyl-ACP synthase, plus other well known fatty acid biosynthetic activities. Other possibilities are genes that encode proteins that do not possess enzymatic activity such as acyl carrier protein. Additional examples include 2-acetyltransferase, oleosin pyruvate dehydrogenase complex, acetyl CoA synthetase, ATP citrate lyase, ADP-glucose pyrophosphorylase and genes of the carnitine-CoA- acetyl-CoA shuttles. It is anticipated that expression of genes related to oil biosynthesis will be targeted to the plastid, using a plastid transit peptide sequence and preferably expressed in the seed embryo. Genes may be introduced that alter the balance of fatty acids present in the oil providing a more healthful or nutritive feedstuff. The introduced DNA may also encode sequences that block expression of enzymes involved in fatty acid biosynthesis, altering the proportions of fatty acids present in the grain such as described below.

Genes may be introduced that enhance the nutritive value of the starch component of the grain, for example by increasing the degree of branching, resulting in improved utilization of the starch in cows by delaying its metabolism.

Besides affecting the major constituents of the grain, genes may be introduced that affect a variety of other nutritive, processing, or other quality aspects of the grain as used for feed or food. For example, pigmentation of the grain may be increased or decreased. Enhancement and stability of yellow pigmentation is desirable in some animal feeds and may be achieved by introduction of genes that result in enhanced production of xanthophylls and carotenes by eliminating rate-limiting steps in their production. Such genes may encode altered

forms of the enzymes phytoene synthase, phytoene desaturase, or lycopene synthase.

Alternatively, unpigmented white corn is desirable for production of many food products and may be produced by the introduction of DNA which blocks or eliminates steps in pigment production pathways.

5           Feed or food comprising some cereal grains possesses insufficient quantities of vitamins and must be supplemented to provide adequate nutritive value. Introduction of genes that enhance vitamin biosynthesis in seeds may be envisioned including, for example, vitamins A, E, B<sub>12</sub>, choline, and the like. For example, maize grain also does not possess sufficient mineral content for optimal nutritive value. Genes that affect the accumulation or availability of  
10       compounds containing phosphorus, sulfur, calcium, manganese, zinc, and iron among others would be valuable. An example may be the introduction of a gene that reduced phytic acid production or encoded the enzyme phytase which enhances phytic acid breakdown. These genes would increase levels of available phosphate in the diet, reducing the need for supplementation with mineral phosphate.

15           Numerous other examples of improvement of cereals for feed and food purposes might be described. The improvements may not even necessarily involve the grain, but may, for example, improve the value of the grain for silage. Introduction of DNA to accomplish this might include sequences that alter lignin production such as those that result in the "brown midrib" phenotype associated with superior feed value for cattle.

20           In addition to direct improvements in feed or food value, genes may also be introduced which improve the processing of grain and improve the value of the products resulting from the processing. The primary method of processing certain grains such as maize is via wetmilling. Maize may be improved through the expression of novel genes that increase the efficiency and reduce the cost of processing such as by decreasing steeping time.

25           Improving the value of wetmilling products may include altering the quantity or quality of starch, oil, corn gluten meal, or the components of corn gluten feed. Elevation of starch may be achieved through the identification and elimination of rate limiting steps in starch biosynthesis or by decreasing levels of the other components of the grain resulting in proportional increases in starch. An example of the former may be the introduction of genes  
30       encoding ADP-glucose pyrophosphorylase enzymes with altered regulatory activity or which



are expressed at higher level. Examples of the latter may include selective inhibitors of, for example, protein or oil biosynthesis expressed during later stages of kernel development.

The properties of starch may be beneficially altered by changing the ratio of amylose to amylopectin, the size of the starch molecules, or their branching pattern. Through these changes a broad range of properties may be modified which include, but are not limited to, changes in gelatinization temperature, heat of gelatinization, clarity of films and pastes, Theological properties, and the like. To accomplish these changes in properties, genes that encode granule-bound or soluble starch synthase activity or branching enzyme activity may be introduced alone or combination. DNA such as antisense constructs may also be used to decrease levels of endogenous activity of these enzymes. The introduced genes or constructs may possess regulatory sequences that time their expression to specific intervals in starch biosynthesis and starch granule development. Furthermore, it may be advisable to introduce and express genes that result in the *in vivo* derivatization, or other modification, of the glucose moieties of the starch molecule. The covalent attachment of any molecule may be envisioned, limited only by the existence of enzymes that catalyze the derivatizations and the accessibility of appropriate substrates in the starch granule. Examples of important derivations may include the addition of functional groups such as amines, carboxyls, or phosphate groups which provide sites for subsequent *in vitro* derivatizations or affect starch properties through the introduction of ionic charges. Examples of other modifications may include direct changes of the glucose units such as loss of hydroxyl groups or their oxidation to aldehyde or carboxyl groups.

Oil is another product of wetmilling of corn and other grains, the value of which may be improved by introduction and expression of genes. The quantity of oil that can be extracted by wetmilling may be elevated by approaches as described for feed and food above. Oil properties may also be altered to improve its performance in the production and use of cooking oil, shortenings, lubricants or other oil-derived products or improvement of its health attributes when used in the food-related applications. Novel fatty acids may also be synthesized which upon extraction can serve as starting materials for chemical syntheses. The changes in oil properties may be achieved by altering the type, level, or lipid arrangement of the fatty acids present in the oil. This in turn may be accomplished by the addition of genes that encode enzymes that catalyze the synthesis of novel fatty acids and the lipids possessing them or by

increasing levels of native fatty acids while possibly reducing levels of precursors.

Alternatively DNA sequences may be introduced which slow or block steps in fatty acid biosynthesis resulting in the increase in precursor fatty acid intermediates. Genes that might be added include desaturases, epoxidases, hydratases, dehydratases, and other enzymes that catalyze reactions involving fatty acid intermediates. Representative examples of catalytic steps that might be blocked include the desaturations from stearic to oleic acid and oleic to linolenic acid resulting in the respective accumulations of stearic and oleic acids.

Improvements in the other major cereal wetmilling products, gluten meal and gluten feed, may also be achieved by the introduction of genes to obtain novel plants. Representative possibilities include but are not limited to those described above for improvement of food and feed value.

In addition it may further be considered that the plant be used for the production or manufacturing of useful biological compounds that were either not produced at all, or not produced at the same level, in the plant previously. The novel plants producing these compounds are made possible by the introduction and expression of genes by transformation methods. The possibilities include, but are not limited to, any biological compound which is presently produced by any organism such as proteins, nucleic acids, primary and intermediary metabolites, carbohydrate polymers, etc. The compounds may be produced by the plant, extracted upon harvest and/or processing, and used for any presently recognized useful purpose such as pharmaceuticals, fragrances, industrial enzymes to name a few.

Further possibilities to exemplify the range of grain traits or properties potentially encoded by introduced genes in transgenic plants include grain with less breakage susceptibility for export purposes or larger grit size when processed by dry milling through introduction of genes that enhance gamma-zein synthesis, popcorn with improved popping quality and expansion volume through genes that increase pericarp thickness, corn with whiter grain for food uses through introduction of genes that effectively block expression of enzymes involved in pigment production pathways, and improved quality of alcoholic beverages or sweet corn through introduction of genes which affect flavor such as the shrunken gene (encoding sucrose synthase) for sweet corn.

Two of the factors determining where plants can be grown are the average daily temperature during the growing season and the length of time between frosts. Within the areas

where it is possible to grow a particular plant, there are varying limitations on the maximal time it is allowed to grow to maturity and be harvested. The plant to be grown in a particular area is selected for its ability to mature and dry down to harvestable moisture content within the required period of time with maximum possible yield. Therefore, plant of varying maturities  
5 are developed for different growing locations. Apart from the need to dry down sufficiently to permit harvest is the desirability of having maximal drying take place in the field to minimize the amount of energy required for additional drying post-harvest. Also the more readily the grain can dry down, the more time there is available for growth and kernel fill. Genes that influence maturity and/or dry down can be identified and introduced into plant lines using  
10 transformation techniques to create new varieties adapted to different growing locations or the same growing location but having improved yield to moisture ratio at harvest. Expression of genes that are involved in regulation of plant development may be especially useful, e.g., the liguleless and rough sheath genes that have been identified in plants.

Genes may be introduced into plants that would improve standability and other plant  
15 growth characteristics. For example, expression of novel genes which confer stronger stalks, improved root systems, or prevent or reduce ear droppage would be of great value to the corn farmer. Introduction and expression of genes that increase the total amount of photoassimilate available by, for example, increasing light distribution and/or interception would be advantageous. In addition the expression of genes that increase the efficiency of  
20 photosynthesis and/or the leaf canopy would further increase gains in productivity. Such approaches would allow for increased plant populations in the field.

Delay of late season vegetative senescence would increase the flow of assimilate into the grain and thus increase yield. Overexpression of genes within plants that are associated with "stay green" or the expression of any gene that delays senescence would achieve be  
25 advantageous. For example, a non-yellowing mutant has been identified in *Festuca pratensis* (Davies et al., 1990). Expression of this gene as well as others may prevent premature breakdown of chlorophyll and thus maintain canopy function.

The ability to utilize available nutrients and minerals may be a limiting factor in growth of many plants. It is proposed that it would be possible to alter nutrient uptake, tolerate pH  
30 extremes, mobilization through the plant, storage pools, and availability for metabolic activities by the introduction of novel genes. These modifications would allow a plant to more

efficiently utilize available nutrients. It is contemplated that an increase in the activity of, for example, an enzyme that is normally present in the plant and involved in nutrient utilization would increase the availability of a nutrient. An example of such an enzyme would be phytase. It is also contemplated that expression of a novel gene may make a nutrient source available  
5 that was previously not accessible, e.g., an enzyme that releases a component of nutrient value from a more complex molecule, perhaps a macromolecule.

Male sterility is useful in the production of hybrid seed. It is proposed that male sterility may be produced through expression of novel genes. For example, it has been shown that expression of genes that encode proteins that interfere with development of the male  
10 inflorescence and/or gametophyte result in male sterility. Chimeric ribonuclease genes that express in the anthers of transgenic tobacco and oilseed rape have been demonstrated to lead to male sterility (Mariani et al, 1990).

For example, a number of mutations were discovered in maize that confer cytoplasmic male sterility. One mutation in particular, referred to as T cytoplasm, also correlates with  
15 sensitivity to Southern corn leaf blight. A DNA sequence, designated TURF-13 (Levings, 1990), was identified that correlates with T cytoplasm. It would be possible through the introduction of TURF-13 via transformation to separate male sterility from disease sensitivity. As it is necessary to be able to restore male fertility for breeding purposes and for grain production, it is proposed that genes encoding restoration of male fertility may also be  
20 introduced.

Introduction of genes encoding traits that can be selected against may be useful for eliminating undesirable linked genes. When two or more genes are introduced together by cotransformation, the genes will be linked together on the host chromosome. For example, a gene encoding a *Bt* gene that confers insect resistance on the plant may be introduced into a  
25 plant together with a *bar* gene that is useful as a selectable marker and confers resistance to the herbicide Ignite® on the plant. However, it may not be desirable to have an insect resistant plant that is also resistant to the herbicide Ignite®. It is proposed that one could also introduce an antisense *bar* gene that is expressed in those tissues where one does not want expression of the *bar* gene, e.g., in whole plant parts. Hence, although the *bar* gene is  
30 expressed and is useful as a selectable marker, it is not useful to confer herbicide resistance on the whole plant. The *bar* antisense gene is a negative selectable marker.

Negative selection is necessary in order to screen a population of transformants for rare homologous recombinants generated through gene targeting. For example, a homologous recombinant may be identified through the inactivation of a gene that was previously expressed in that cell. The antisense gene to neomycin phosphotransferase II (*nptII*) has been  
5 investigated as a negative selectable marker in tobacco (*Nicotiana tabacum*) and *Arabidopsis thaliana* (Xiang and Guerra, 1993). In this example both sense and antisense *nptII* genes are introduced into a plant through transformation and the resultant plants are sensitive to the antibiotic kanamycin. An introduced gene that integrates into the host cell chromosome at the site of the antisense *nptII* gene, and inactivates the antisense gene, will make the plant resistant  
10 to kanamycin and other aminoglycoside antibiotics. Therefore, rare site specific recombinants may be identified by screening for antibiotic resistance. Similarly, any gene, native to the plant or introduced through transformation, that when inactivated confers resistance to a compound, may be useful as a negative selectable marker.

It is contemplated that negative selectable markers may also be useful in other ways.  
15 One application is to construct transgenic lines in which one could select for transposition to unlinked sites. In the process of tagging it is most common for the transposable element to move to a genetically linked site on the same chromosome. A selectable marker for recovery of rare plants in which transposition has occurred to an unlinked locus would be useful. For example, the enzyme cytosine deaminase may be useful for this purpose (Stouggard, 1993). In  
20 the presence of this enzyme the compound 5-fluorocytosine is converted to 5-fluoruracil which is toxic to plant and animal cells. If a transposable element is linked to the gene for the enzyme cytosine deaminase, one may select for transposition to unlinked sites by selecting for transposition events in which the resultant plant is now resistant to 5-fluorocytosine. The parental plants and plants containing transpositions to linked sites will remain sensitive to 5-  
25 fluorocytosine. Resistance to 5-fluorocytosine is due to loss of the cytosine deaminase gene through genetic segregation of the transposable element and the cytosine deaminase gene. Other genes that encode proteins that render the plant sensitive to a certain compound will also be useful in this context. For example, T-DNA gene 2 from *Agrobacterium tumefaciens* encodes a protein that catalyzes the conversion of alpha-naphthalene acetamide (NAM) to  
30 alpha-naphthalene acetic acid (NAA) renders plant cells sensitive to high concentrations of NAM (Depicker et al., 1988).

It is also contemplated that negative selectable markers may be useful in the construction of transposon tagging lines. For example, by marking an autonomous transposable element such as Ac, Master Mu, or En/Spn with a negative selectable marker, one could select for transformants in which the autonomous element is not stably integrated into the genome. This would be desirable, for example, when transient expression of the autonomous element is desired to activate in *trans* the transposition of a defective transposable element, such as Ds, but stable integration of the autonomous element is not desired. The presence of the autonomous element may not be desired in order to stabilize the defective element, i.e., prevent it from further transposing. However, it is proposed that if stable integration of an autonomous transposable element is desired in a plant the presence of a negative selectable marker may make it possible to eliminate the autonomous element during the breeding process. DNA may be introduced into plants for the purpose of expressing RNA transcripts that function to affect plant phenotype yet are not translated into protein. Two examples are antisense RNA and RNA with ribozyme activity. Both may serve possible functions in reducing or eliminating expression of native or introduced plant genes.

Genes may be constructed or isolated, which when transcribed, produce antisense RNA that is complementary to all or part(s) of a targeted messenger RNA(s). The antisense RNA reduces production of the polypeptide product of the messenger RNA. The polypeptide product may be any protein encoded by the plant genome. The aforementioned genes will be referred to as antisense genes. An antisense gene may thus be introduced into a plant by transformation methods to produce a novel transgenic plant with reduced expression of a selected protein of interest. For example, the protein may be an enzyme that catalyzes a reaction in the plant. Reduction of the enzyme activity may reduce or eliminate products of the reaction which include any enzymatically synthesized compound in the plant such as fatty acids, amino acids, carbohydrates, nucleic acids and the like. Alternatively, the protein may be a storage protein, such as a zein, or a structural protein, the decreased expression of which may lead to changes in seed amino acid composition or plant morphological changes respectively. The possibilities cited above are provided only by way of example and do not represent the full range of applications.

Genes may also be constructed or isolated, which when transcribed produce RNA enzymes, or ribozymes, which can act as endoribonucleases and catalyze the cleavage of RNA

molecules with selected sequences. The cleavage of selected messenger RNA's can result in the reduced production of their encoded polypeptide products. These genes may be used to prepare novel transgenic plants which possess them. The transgenic plants may possess reduced levels of polypeptides including but not limited to the polypeptides cited above that may be affected by antisense RNA.

It is also possible that genes may be introduced to produce novel transgenic plants which have reduced expression of a native gene product by a mechanism of cosuppression. It has been demonstrated in tobacco, tomato, and petunia (Goring et al, 1991; Smith et al., 1990; Napoli et al., 1990; van der Krol et al., 1990) that expression of the sense transcript of a native gene will reduce or eliminate expression of the native gene in a manner similar to that observed for antisense genes. The introduced gene may encode all or part of the targeted native protein but its translation may not be required for reduction of levels of that native protein.

For example, DNA elements including those of transposable elements such as Ds, Ac, or Mu, may be inserted into a gene and cause mutations. These DNA elements may be inserted in order to inactivate (or activate) a gene and thereby "tag" a particular trait. In this instance the transposable element does not cause instability of the tagged mutation, because the utility of the element does not depend on its ability to move in the genome. Once a desired trait is tagged, the introduced DNA sequence may be used to clone the corresponding gene, e.g., using the introduced DNA sequence as a PCR primer together with PCR gene cloning techniques (Shapiro, 1983; Dellaporta et al., 1988). Once identified, the entire gene(s) for the particular trait, including control or regulatory regions where desired may be isolated, cloned and manipulated as desired. The utility of DNA elements introduced into an organism for purposed of gene tagging is independent of the DNA sequence and does not depend on any biological activity of the DNA sequence, i.e., transcription into RNA or translation into protein. The sole function of the DNA element is to disrupt the DNA sequence of a gene.

It is contemplated that unexpressed DNA sequences, including novel synthetic sequences could be introduced into cells as proprietary "labels" of those cells and plants and seeds thereof. It would not be necessary for a label DNA element to disrupt the function of a gene endogenous to the host organism, as the sole function of this DNA would be to identify the origin of the organism. For example, one could introduce a unique DNA sequence into a plant and this DNA element would identify all cells, plants, and progeny of these cells as

having arisen from that labeled source. It is proposed that inclusion of label DNAs would enable one to distinguish proprietary germplasm or germplasm derived from such, from unlabelled germplasm.

Another possible element which may be introduced is a matrix attachment region element (MAR), such as the chicken lysozyme A element (Stief et al., 1989), which can be positioned around an expressible gene of interest to effect an increase in overall expression of the gene and diminish position dependant effects upon incorporation into the plant genome (Stief et al., 1989; Phi-Van et al., 1990).

Plant species may be transformed with the DNA construct of the present invention by the DNA-mediated transformation of plant cell protoplasts and subsequent regeneration of the plant from the transformed protoplasts in accordance with procedures well known in the art.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and utilane meristem).

Plants of the present invention may take a variety of forms. The plants may be chimeras of transformed cells and non-transformed cells; the plants may be clonal transformants (e.g., all cells transformed to contain the expression cassette); the plants may comprise grafts of transformed and untransformed tissues (e.g., a transformed root stock grafted to an untransformed scion in citrus species). The transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, first generation (or T1) transformed plants may be selfed to give homozygous second generation (or T2) transformed plants, and the T2 plants further



propagated through classical breeding techniques. A dominant selectable marker (such as npt II) can be associated with the expression cassette to assist in breeding.

Thus, the present invention provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including a transformed plastid or other organelle, e.g., nucleus, mitochondria or chloroplast. The present invention may be used for transformation of any plant species, including, but not limited to, cells from corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea utilane*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, duckweed (*Lemna*), barley, vegetables, ornamentals, and conifers.

Duckweed (*Lemna*, see WO 00/07210) includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. Angusta*, *Wa. Arrhiza*, *Wa. Australina*, *Wa. Borealis*, *Wa. Brasiliensis*, *Wa. Columbiana*, *Wa. Elongata*, *Wa. Globosa*, *Wa. Microscopica*, *Wa. Neglecta*) and genus *Wofieldia* (*Wl. utila*, *Wl. utilanen*, *Wl. gladiata*, *Wl. utila*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred; with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic

scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae – A Monograph Study. Geobotanisches Institut ETH, Stiftung Rubel, Zurich (1986)).

Vegetables within the scope of the invention include tomatoes (*Lycopersicon*  
 5 *esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*).  
 Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*),  
 hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus*  
 10 spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga utilane*);  
 15 Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not  
 20 limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo. Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and  
 25 redtop.

Other plants within the scope of the invention include *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine,  
 30 triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant,

pepper, cauliflower, Brassica, e.g., broccoli, cabbage, utilian sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, utiliane, and zucchini.

Ornamental plants within the scope of the invention include impatiens, Begonia,  
5 Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other plants within the scope of the invention are shown in Table 1 (above).

Preferably, transgenic plants of the present invention are crop plants and in particular  
10 cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn, rice and soybean.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with  
15 the expression cassettes of the present invention. Numerous transformation vectors are available for plant transformation, and the expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

A variety of techniques are available and known to those skilled in the art for  
20 introduction of constructs into a plant cell host. These techniques generally include transformation with DNA employing *A. tumefaciens* or *A. rhizogenes* as the transforming agent, liposomes, PEG precipitation, electroporation, DNA injection, direct DNA uptake, microprojectile bombardment, particle acceleration, and the like (See, for example, EP 295959 and EP 138341) (see below). However, cells other than plant cells may be transformed with  
25 the expression cassettes of the invention. The general descriptions of plant expression vectors and reporter genes, and *Agrobacterium* and *Agrobacterium*-mediated gene transfer, can be found in Gruber et al. (1993).

Expression vectors containing genomic or synthetic fragments can be introduced into protoplasts or into intact tissues or isolated cells. Preferably expression vectors are introduced  
30 into intact tissue. General methods of culturing plant tissues are provided for example by Maki et al., (1993); and by Phillips et al. (1988). Preferably, expression vectors are introduced into

maize or other plant tissues using a direct gene transfer method such as microprojectile-mediated delivery, DNA injection, electroporation and the like. More preferably expression vectors are introduced into plant tissues using the microprojectile media delivery with the biolistic device. See, for example, Tomes et al. (1995). The vectors of the invention can not  
5 only be used for expression of structural genes but may also be used in exon-trap cloning, or promoter trap procedures to detect differential gene expression in varieties of tissues, (Lindsey et al., 1993; Auch & Reth et al.).

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium* spp. Ti-derived vectors transform a wide variety of higher plants, including  
10 monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Park et al., 1985; Hiei et al., 1994). The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An et al., 1985). For introduction into plants, the chimeric genes of the invention can be inserted into binary vectors  
15 as described in the examples.

Other transformation methods are available to those skilled in the art, such as direct uptake of foreign DNA constructs (see EP 295959), techniques of electroporation (Fromm et al., 1986) or high velocity ballistic bombardment with metal particles coated with the nucleic acid constructs (Kline et al., 1987, and U.S. Patent No. 4,945,050). Once transformed, the  
20 cells can be regenerated by those skilled in the art. Of particular relevance are the recently described methods to transform foreign genes into commercially important crops, such as rapeseed (De Block et al., 1989), sunflower (Everett et al., 1987), soybean (McCabe et al., 1988; Hinchey et al., 1988; Chee et al., 1989; Christou et al., 1989; EP 301749), rice (Hiei et al., 1994), and corn (Gordon Kamm et al., 1990; Fromm et al., 1990).

Those skilled in the art will appreciate that the choice of method might depend on the  
25 type of plant, i.e., monocotyledonous or dicotyledonous, targeted for transformation. Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), electroporation (Riggs et al., 1986), *Agrobacterium*-mediated transformation (Hinchey et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle  
30 acceleration using devices available from Agracetus, Inc., Madison, Wis. And BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al.,

1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat). In one embodiment, the protoplast transformation method for maize is employed (European Patent Application EP 0 292 435, U. S. Pat. No. 5,350,689).

In another embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994. The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3N-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand

copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplasmic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

*Agrobacterium tumefaciens* cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known.

For example, vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, 1984). In one preferred embodiment, the expression cassettes of the present invention may be inserted into either of the binary vectors pCIB200 and pCIB2001 for use with *Agrobacterium*. These vector cassettes for *Agrobacterium*-mediated transformation were constructed in the following manner. PTJS75kan was created by NarI digestion of pTJS75 (Schmidhauser & Helinski, 1985) allowing excision of the tetracycline-resistance gene, followed by insertion of an AccI fragment from pUC4K carrying an NPTII (Messing & Vierra, 1982; Bevan et al., 1983; McBride et al., 1990). XhoI linkers were ligated to the EcoRV fragment of pCIB7 which contains the left and right T-DNA borders, a plant selectable nos/nptII chimeric gene and the pUC polylinker (Rothstein et al., 1987), and the XhoI-digested fragment was cloned into SalI-digested pTJS75kan to create pCIB200 (see also EP 0 332 104, example 19). PCIB200 contains the following unique polylinker restriction sites: EcoRI, SstI, KpnI, BglII, XbaI, and SalI. The plasmid pCIB2001 is a derivative of pCIB200 which was created by the insertion into the polylinker of additional restriction sites. Unique restriction sites in the polylinker of pCIB2001 are EcoRI, SstI, KpnI, BglII, XbaI, SalI, MluI, BclI, AvrII, ApaI, HpaI, and StuI. PCIB2001, in addition to containing these unique restriction sites also has plant and bacterial kanamycin selection, left and right T-DNA borders for

*Agrobacterium*-mediated transformation, the RK2-derived trfA function for mobilization between *E. coli* and other hosts, and the OriT and OriV functions also from RK2. The pCIB2001 polylinker is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

5       An additional vector useful for *Agrobacterium*-mediated transformation is the binary vector pCIB 10, which contains a gene encoding kanamycin resistance for selection in plants, T-DNA right and left border sequences and incorporates sequences from the wide host- range plasmid pRK252 allowing it to replicate in both *E. coli* and *Agrobacterium*. Its construction is described by Rothstein et al., 1987. Various derivatives of pCIB10 have been constructed  
10       which incorporate the gene for hygromycin B phosphotransferase described by Gritz et al., 1983. These derivatives enable selection of transgenic plant cells on hygromycin only (pCIB743), or hygromycin and kanamycin (pCIB715, pCIB717).

      Methods using either a form of direct gene transfer or *Agrobacterium*-mediated transfer usually, but not necessarily, are undertaken with a selectable marker which may  
15       provide resistance to an antibiotic (e.g., kanamycin, hygromycin or methotrexate) or a herbicide (e.g., phosphinothricin). The choice of selectable marker for plant transformation is not, however, critical to the invention.

      For certain plant species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the nptII gene which  
20       confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982; Bevan et al., 1983), the bar gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the hph gene which confers resistance to the antibiotic hygromycin (Blochinger & Diggelmann), and the dhfr gene, which confers resistance to methotrexate (Bourouis et al., 1983).

25       One such vector useful for direct gene transfer techniques in combination with selection by the herbicide Basta (or phosphinothricin) is pCIB3064. This vector is based on the plasmid pCIB246, which comprises the CaMV 35S promoter in operational fusion to the *E. coli* GUS gene and the CaMV 35S transcriptional terminator and is described in the PCT published application WO 93/07278, herein incorporated by reference. One gene useful for conferring  
30       resistance to phosphinothricin is the bar gene from *Streptomyces viridochromogenes*

(Thompson et al., 1987). This vector is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

An additional transformation vector is pSOG35 which utilizes the *E. coli* gene dihydrofolate reductase (DHFR) as a selectable marker conferring resistance to methotrexate.

5 PCR was used to amplify the 35S promoter (about 800 bp), intron 6 from the maize Adh1 gene (about 550 bp) and 18 bp of the GUS untranslated leader sequence from pSOG10. A 250 bp fragment encoding the *E. coli* dihydrofolate reductase type II gene was also amplified by PCR and these two PCR fragments were assembled with a SacI-PstI fragment from pBI221 (Clontech) which comprised the pUC19 vector backbone and the nopaline synthase terminator.  
10 Assembly of these fragments generated pSOG19 which contains the 35S promoter in fusion with the intron 6 sequence, the GUS leader, the DHFR gene and the nopaline synthase terminator. Replacement of the GUS leader in pSOG19 with the leader sequence from Maize Chlorotic Mottle Virus check (MCMV) generated the vector pSOG35. pSOG19 and pSOG35 carry the pUC-derived gene for ampicillin resistance and have HindIII, SphI, PstI and EcoRI  
15 sites available for the cloning of foreign sequences.

Transgenic plant cells are then placed in an appropriate selective medium for selection of transgenic cells which are then grown to callus. Shoots are grown from callus and plantlets generated from the shoot by growing in rooting medium. The various constructs normally will be joined to a marker for selection in plant cells. Conveniently, the marker may be resistance  
20 to a biocide (particularly an antibiotic, such as kanamycin, G418, bleomycin, hygromycin, chloramphenicol, herbicide, or the like). The particular marker used will allow for selection of transformed cells as compared to cells lacking the DNA which has been introduced. Components of DNA constructs including transcription cassettes of this invention may be prepared from sequences which are native (endogenous) or foreign (exogenous) to the host.  
25 By "foreign" it is meant that the sequence is not found in the wild-type host into which the construct is introduced. Heterologous constructs will contain at least one region which is not native to the gene from which the transcription-initiation-region is derived.

To confirm the presence of the transgenes in transgenic cells and plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well  
30 known to those of skill in the art, such as Southern and Northern blotting, *in situ* hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays,



such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

5 DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The presence of nucleic acid elements introduced through the methods of this invention  
10 may be determined by polymerase chain reaction (PCR). Using this technique discrete fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to  
15 determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of  
20 transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected  
25 DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

Both PCR and Southern hybridization techniques can be used to demonstrate  
5 transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The nonchimeric nature of the callus and the parental transformants ( $R_0$ ) was suggested by germline transmission and the identical Southern blot hybridization patterns and  
10 intensities of the transforming DNA in callus,  $R_0$  plants and  $R_1$  progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used  
15 for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA  
20 product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

25 While Southern blotting and PCR may be used to detect the preselected DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

30 Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-

chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or denaturing gel electrophoresis or isoelectric focusing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic

descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed; increased vitamin, amino acid, and antioxidant content; the production of antibodies (passive immunization) and nutraceuticals), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. Additionally, the use of root-specific promoters in transgenic plants can provide beneficial traits that are localized in the consumable (by animals and humans) roots of plants such as carrots, parsnips, and beets. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of drought, disease, or other stresses. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, utilane breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines.

Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-339, 358-366, 441-515, 517-529, 536-579 and 601-773, as well as complementary, ortholog, and variant sequences thereof.

Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

The invention will be further described by the following non-limiting examples.

## **EXAMPLES**

### **Example 1**      GeneChip® Standard Protocol

#### **Quantitation of total RNA**

Total RNA from plant tissue is extracted and quantified.

#### 1. Quantify total RNA using GeneQuant

$1\text{OD}_{260}=40\text{ ug RNA/ml}$ ;  $A_{260}/A_{280}=1.9$  to about 2.1

2. Run gel to check the integrity and purity of the extracted RNA

#### Synthesis of double-stranded cDNA

Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019) was employed to prepare cDNAs. T7-(dT)<sub>24</sub> oligonucleotides were prepared and purified by HPLC. (5'-GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)<sub>24</sub>-3'; SEQ ID NO:584).

##### Step 1. Primer hybridization:

Incubate at 70°C for 10 minutes

10 Quick spin and put on ice briefly

##### Step 2. Temperature adjustment:

Incubate at 42°C for 2 minutes

##### Step 3. First strand synthesis:

15 DEPC-water- 1 ul  
RNA (10 ug final)-10 ul  
T7=(dT)<sub>24</sub> Primer (100 pmol final)-1 ul pmol  
5X 1<sup>st</sup> strand cDNA buffer-4 ul  
0.1M DTT (10 mM final)- 2 ul  
10 mM dNTP mix (500 uM final)-1 ul  
20 Superscript II RT 200 U/ul- 1 ul  
Total of 20 ul

Mix well

Incubate at 42°C for 1 hour

##### Step 4. Second strand synthesis:

25 Place reactions on ice, quick spin  
DEPC-water- 91 ul  
5X 2<sup>nd</sup> strand cDNA buffer- 30 ul  
10 mM dNTP mix (250 mM final) – 3 ul  
*E. coli* DNA ligase (10 U/ul)-1 ul  
30 *E. coli* DNA polymerase 1-10 U/ul- 4 ul

RnaseH 2U/ul -1 ul  
 T4 DNA polymerase 5 U/ul-2 ul  
 0.5 M EDTA (0.5 M final)—10 ul  
 Total 162 ul

5 Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- 10 1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime Inc., pI-188233) at 14,000X,  
 transfer 162 ul of cDNA to PLG
2. Add 162 ul of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge 2 minutes
3. Transfer the supernatant to a fresh 1.5 ml tube, add
- |    |                                      |     |
|----|--------------------------------------|-----|
|    | Glycogen (5 mg/ml)                   | 2   |
| 15 | 0.5 M NH <sub>4</sub> OAC (0.75xVol) | 120 |
|    | ETOH (2.5xVol, -20°C)                | 400 |
4. Mix well and centrifuge at 14,000X for 20 minutes
5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
- 20 7. Add 44 ul DEPC H<sub>2</sub>O

Analyze of quantity and size distribution of cDNA

Run a gel using 1 ul of the double-stranded synthesis product

Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

- |    |                              |             |
|----|------------------------------|-------------|
| 25 | Purified cDNA                | 22 ul       |
|    | 10X Hy buffer                | 4 ul        |
|    | 10X biotin ribonucleotides   | 4 ul        |
|    | 10X DTT                      | 4 ul        |
|    | 10X Rnase inhibitor mix      | 4 ul        |
| 30 | <u>20X T7 RNA polymerase</u> | <u>2 ul</u> |



Total 40 ul

Centrifuge 5 seconds, and incubate for 4 hours at 37°C

Gently mix every 30-45 minutes

5 Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

cRNA 40 ul

DEPC H<sub>2</sub>O 60 ul

RLT buffer 350 ul mix by vortexing

10 EtOH 250 ul mix by pipetting

Total 700 ul

Wait 1 minute or more for the RNA to stick

Centrifuge at 2000 rpm for 5 minutes

RPE buffer 500 ul

15 Centrifuge at 10,000 rpm for 1 minute

RPE buffer 500 ul

Centrifuge at 10,000 rpm for 1 minute

Centrifuge at 10,000 rpm for 1 minute to dry the column

DEPC H<sub>2</sub>O 30 ul

20 Wait for 1 minute, then elute cRNA from by centrifugation, 10K 1 minute

DEPC H<sub>2</sub>O 30 ul

Repeat previous step

Determine concentration and dilute to 1 ug/ul concentration

25 Fragmentation of cRNA

cRNA (1 ug/ul) 15 ul

5X Fragmentation Buffer\* 6 ul

DEPC H<sub>2</sub>O 9 ul

30 ul

30

\*5x Fragmentation Buffer

	1M Tris (pH8.1)	4.0 ml
	MgOAc	0.64 g
	KOAC	0.98 g
5	DEPC H <sub>2</sub> O	
	Total	20 ml
	Filter Sterilize	

Array wash and staining

10 Stringent Wash Buffer\*\*

Non-Stringent Wash Buffer\*\*\*

SAPE Stain\*\*\*\*

Antibody Stain\*\*\*\*\*

15 Wash on fluidics station using the appropriate antibody amplification protocol

\*\*Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H<sub>2</sub>O 910 ml,

Filter Sterilize

\*\*\*Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H<sub>2</sub>O 698 ml, Filter

20 Sterilize, Antifoam 1.0.

\*\*\*\*SAPE stain: 2X Stain Buffer 600 ul, BSA 48 ul, SAPE 12ul, H<sub>2</sub>O 540 ul.\*\*\*\*\*Antibody Stain: 2X Stain Buffer 300 ul, H<sub>2</sub>O 266.4 ul, BSA 24 ul, Goat IgG 6 ul,

Biotinylated Ab 3.6 ul

25 **Example 2**      Characterization of Gene Expression Profiles During Plant Development  
using the GeneChip

The *Arabidopsis* GeneChip provides a method to simultaneously scan over 30% of the genome for the expression profile of each gene on chip. By using RNA extracted from different tissue and developmental stages of development, a scan of the entire *Arabidopsis* plant is achieved.

30 The advantages of a gene chip in such an analysis include a global gene expression analysis,

quantitative results, a highly reproducible system, and a higher sensitivity than Northern blot analyses. Moreover, a gene chip with *Arabidopsis* DNA has a further advantage in that the *Arabidopsis* genome is well characterized.

Using the recently designed *Arabidopsis* high density oligonucleotide probe array, a total of 8,100 *Arabidopsis thaliana* genes were surveyed for temporal and developmental expression profiling. The objective was to identify known and novel genes that are expressed in specific organs (spatial expression) or developmental stages (temporal expression versus constitutive expression). The represented genes included approximately 1,000 known full length cDNAs, a collection of approximately 500 ESTs or full length sequences, 3,500 annotated Genbank genomic sequences (the transcripts of which were confirmed by the presence of ESTs in the database) and about 3,700 annotated Genbank sequences with a predicted translated open reading frame with 2 or more "hits" with a protein in the protein database having a defined function.

Total RNA was isolated from 9 samples at different developmental stages for to prepare cRNA microanalysis. These samples were analyzed in 9 separate GeneChip® (see, e.g., U.S. Patent Nos. 5,445,934, 5,744,305, 5,700,305, 5,700,637, 5,945,334 and EP 619321 and EP 373203) experiments that included RNA from: 1) germinating seed, day 4; 2) root 2 week; 3) root adult; 4) leaf; 5) leaf adult; 6) leaf senescence; 7) stem; 8) immature siliques; and 9) flowers prior to pollen shed. The samples were hybridized to the *Arabidopsis* arrays and analyzed by laser scanning for relative expression level, fold difference, organ and developmental expression. All genes were expressed in at least one of the samples.

Seeds of wild-type plants of *Arabidopsis thaliana*, ecotype Columbia, were sterilized and germinated in soil. Plants were grown in conviron growth chambers with 12 hours of light at 22°C 12:12 light dark cycle in metromix. Samples from leaves of 2-week, 5-week, 6-week, 8-week, and 11-week old plants, and inflorescences, flowers and siliques of the 6-week and 8-week old plants were collected (Table 2). In addition, 4-day old seedlings and roots from 2-week, 4-week, and 5-week old plants cultured in MS liquid medium were collected. Samples collected from over 30 plants were pooled and homogenized in liquid nitrogen. Total RNA was extracted using Qiagen Rneasy column (Qiagen, Chatsworth, CA).

Table 2

	germinating seedling	4 days of development
	germinating seedling	4 days of development
5	leaf	2 weeks after planting
	leaf	2 weeks after planting
	leaf	5 weeks after planting
	leaf	6 weeks after planting
	leaf	8 weeks after planting
10	leaf	11 weeks after planting
	root	2 weeks after planting
	root	2 weeks after planting
	root	5 weeks after planting
	root	6 weeks after planting
15	flower	5 weeks after planting
	flower	6 weeks after planting
	siliques	5 weeks after planting
	siliques	6 weeks after planting
	siliques	8-11 weeks after planting
20	inflorescence	6 weeks after planting
	inflorescence	5 weeks after planting

Total RNA (5 µg) from each sample was reverse transcribed using an oligo dT<sub>(24)</sub> primer containing a 5' T7 RNA polymerase promoter sequence (5'-GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)<sub>24</sub>-3'; SEQ ID NO:585) and SuperScript II reverse transcriptase (Life Technologies). Second strand of cDNA was synthesized using DNA polymerase I and DNA ligase. Biotinylated complementary RNAs (cRNAs) were *in vitro* transcribed by T7 RNA Polymerase (ENZO BioArray High Yield RNA Transcript Labeling Kit, Enzo). cRNAs were purified using an affinity resin (Qiagen Rneasy Spin Columns) and randomly fragmented by incubating at 94° C for 35 minutes in a buffer

containing 40 mM Tris-acetate, pH 8.1, 100 mM potassium acetate, and 30 mM magnesium acetate to produce molecules of approximately 35 to 200 bases.

The labeled samples were denatured at 99° C for 5 minutes, equilibrated at 45°C for 5 minutes, and hybridized to the *Arabidopsis* GeneChip® genome array (Affymetrix) at 45°C for 5  
16 hours on a rotisserie at 60 rpm. The hybridized arrays were then rinsed with 1X STT and stained with streptavidin phycoerythrin at 25°C for 10 minutes twice with a rinse in between. After staining, arrays were washed with 1X STT at 25°C for 20 minutes and stained with biotinylated anti-streptavidin antibody at 25°C for 10 minutes. The probe array was stained with SAPE at 25°C for 10 minutes and washed with wash buffer A at 30°C for 30 minutes.  
10 All of the wash and stain procedures were completed using a fluidic station (Affymetrix). The probe array was scanned twice and the intensities were averaged with a Hewlett-Packard GeneArray Scanner.

Genechip Suite 3.2 (Affymetrix) was used for data normalization. The overall intensity of all probe sets of each chip was scaled to 100 so that the hybridization intensity of all arrays  
15 was equivalent. False positives are defined based on experiments in which samples are split, hybridized to GeneChip® expression arrays and the results compared. A false positive is indicated if a probe set is scored qualitatively as an "Increase" or "Decrease" and quantitatively as changing by at least 2-fold and the average difference is greater than 25. A significant change is defined as 2-fold change or above with an expression baseline of 25, which is  
20 determined as the threshold level according to the scaling. For example, the data from each chip was loaded into GeneSpring software and analyzed for fold differences with the leaf samples. The 2-week leaf samples were used to find genes expressed 4-fold or higher in the leaf sample at 2 weeks of age versus all the other tissues. The remaining leaf samples at 5, 6, 8, and 11 weeks were not analyzed at this stage, but were analyzed independently. The leaf  
25 sample at 5 weeks was also analyzed against all other tissues except the remaining leaf samples for genes expressed 4-fold or higher in leaf tissue at 5 weeks. The other leaf samples were analyzed in a similar fashion. This allowed the selection of genes that were at least 4-fold elevated in expression in a leaf sample in at least one stage of development. When these genes were combined, there were 92 genes that were preferentially expressed in leaf tissue.

### Image analysis and data mining

Two text files are included in the analysis:

- a. One with Absolute analysis: giving the status of each gene, either absent or present in the samples
- 5 b. The other with Comparison analysis: comparing gene expression levels between two samples

### Arabidopsis Genome Array

A high-density *Arabidopsis* oligonucleotide array was used that includes probes for 8,100 *Arabidopsis* genes and 40 probes for spiking and negative controls. For each gene, there are 16 probe pairs (probe sets) including perfect match probes and mismatch probes for non-specific binding control. The *Arabidopsis* genes are represented by known genes, predicted genes and approximately 100 clusters of ESTs. Predicted gene sequences were extracted and confirmed computationally by matching the genome sequence with ESTs and protein sequences.

15 The reproducibility of the array was characterized by calculation of the rate of false changes (number of genes significantly changed over the total number of genes on the array; Lipshultz, 1999). Two cDNA and subsequently cRNA (the antisense RNA synthesized by *in vitro* transcription using cDNAs as templates in the presence of biotinylated ribonucleotides) samples were prepared in parallel from the same total RNA samples, and hybridized to two different arrays manufactured in the same lot or different lots. Genes that showed changes of  $\geq$  2-fold and a signal threshold above the background (calculated according to the setting of the global scaling factor) were counted as false changes. Data from 15 pairs of array experiments indicated that false changes between two experiments using arrays of the same lot is 0.17% (based on 8 pairs), while the false change using arrays of two different lots is 0.22% (based on 20 7 pairs). Further analyses of these genes indicate that the fold change and expression levels are low and close to the threshold (Zhu and Wang, 2000).

Selected housekeeping genes are used to ensure the quality of the array experiments, because the quality of the total RNA and subsequently synthesized cDNA and cRNA samples has direct impact on the array results. Sample quality, specifically, labeled cRNA quality was monitored by comparing the ratio of the hybridization signal of 3N and 5N probe sets for 30

GAPDH and ubiquitin1 1. Only data with a consistent 3N/5N ratio (Zhu and Wang, 2000) was archived in the database and used.

#### Specific Selection Criteria

The following criteria selection were employed to identify *Arabidopsis* genes that were constitutively expressed.

- Baseline (background) = relative expression level of 50
- Candidates were first selected for relative expression of  $\geq 250$  in all tissues for a given gene.
- Relative expression range of the 346 genes which were expressed in all tissue = 250-6,765.
  - Candidate genes were selected for  $\pm 5$  fold difference in expression = 331 genes
  - Candidate genes were selected for  $\pm 3$  fold difference = 276 genes
- For 174 selected genes which met the above criteria

The expression for each gene was averaged:

'low' expression = 250–750; 97 genes (55.7%)

'moderate' expression = 750–2250; 70 genes (40.2%)

'high' expression = 2250–6750; 8 genes (4.6%)

- 47 genes were selected for further analysis

'low' expression = 250–750; 21 genes (44.6%)

'moderate' expression = 750–2250; 24 genes (51.0%)

'high' expression = 2250–6750; 3 genes (6.4%)

The following criteria were used to identify *Arabidopsis* genes expressed primarily in root tissue.

- Baseline (background) = relative expression level of 50
- Candidates were first selected for relative expression of  $\geq 300$  in all tissues for a given gene excluding the germinating seed data.
- Candidate genes were sorted by fold difference. Root  $\pm 3$  other tissue  $<10$  (10 fold lower expression)

- When the germinating seed data included was included with the 64 selected genes 39 were identified with relative expression  $\geq 150$ .
- Thirteen were selected for further analysis.

### **Abundance Distribution of Transcripts**

5 Knowledge of the levels of all detectable mRNA species in *Arabidopsis* is useful for evaluating the complexity of the transcriptome and its control. The abundance of the transcript species and their expression level in 5-week-old *Arabidopsis* was analyzed by examining the mRNA transcripts present in four major organs, leaves, roots, inflorescence stems, and flowers. Among 8,300 genes analyzed, over 5,000 transcript species were detected in each  
10 organ. Comparison of the transcripts presented in these organs revealed the number and percentage of the commonly expressed and specifically expressed transcripts in each organ at this stage (Table 3).

Table 3

	Root	Inflorescence Stem	Leaf	Flower
Root	6,052	4,928	4,915	5,243
Inflorescence Stem		5,399	4,828	5,036
Leaf			5,416	4,995
Flower				6,097
Specific	426	55	89	380

15 Expression measurements (average signal difference between perfect-match probes and mismatch probes) of the genes in each organ were examined. Data were collected and log transformed, then plotted against their frequencies. A normal distribution of the transcript abundance was revealed for all four organs. The median of the distributions is similar to the  
20 profiles of yeast, mammalian, and *E. coli* (Lockhart and Winzler, 2000). Overall, the transcription profile is more complex in flowers than in the vegetative organs. It is evidenced by the elevated frequencies in almost every level of transcription. Root has the most complex profile among the vegetative organs, while leaf and inflorescence stem have very similar and simpler profiles.



## **2. Constitutive and Organ Differential Gene Expression**

The composition of the constitutively and organ differentially expressed transcripts were characterized. A total of 347 constitutive expressed genes with median or high-level transcripts were selected from the commonly expressed gene pool. These genes are constantly  
5 expressed above median expression level (average difference greater than 500) for all organs and developmental stages examined. Functional categorization indicated that majority of the known constitutive genes are involved in metabolism (28%) and ribosomal protein synthesis (15%), followed by genes involving transcription (8%), signaling (6%), transport (5%), membrane (5%), synthases (5%), membrane (5%), and stress and defense related (7%) (Table  
10 8). About 15% of the genes identified have no function assigned.

Organ differential expressed genes were also analyzed. These genes were expressed at median level (average difference greater than 50) in certain organ at all developmental stages, e.g., compared to other organs, the expression level for these genes in the organ are 4-fold higher than others. By these criteria, genes differentially expressed in root (64), leaf (94),  
15 inflorescence stem (3), and flower (36) were identified, and functionally categorized. To examine the organ-specificity of the differential expression, the expression level of differentially expressed genes were plotted against represented samples. The root differential expressed genes are expressed almost exclusively in root and young whole seedlings. There were 51 genes that were expressed only in root. Twenty-three percent of these genes had no known  
20 function while peroxidases and defense genes represented 51% of the genes.

Similar experiments were conducted for root at least 3 hours after exposure to stress, e.g., salt, mannitol or cold (Tables 9-10). Twenty-five root-specific promoters were downregulated and 8 were upregulated in response to salt stress, 21 were downregulated and 17 were upregulated in response to mannitol, and 22 were downregulated and 7 were  
25 upregulated in response to cold. Ten promoters did not respond to any of the stresses.

## **3. Dynamics of Gene Expression During Leaf Development**

In order to examine the dynamics of gene expression at mRNA level during different organ development, genes with transcripts detected in various developmental stages were analyzed. A total of 5,247 genes expressed during leaf development were subject to cluster  
30 analysis. Various clustering methods, including self-organizing map (SOM, Tamayo et al.,

1999), hierarchical cluster (Eisen et al., 1998) and K-mean, generated similar clusters. Sixteen groups of genes formed according to their expression patterns when SOM was used. Four groups of genes were examined in detail.

Cluster 15 shows a group of genes down regulated during leaf development. Genes in this group generally have a very high transcription level. However, they reduce their expression level by least 2-fold toward senescence. Among 34 genes in the cluster, 28 of them were photosynthesis related. Interestingly, some of the genes related to photosynthesis are also found in cluster 6, which shows a more gradual reduction in expression. These genes, such as ferredoxin-NADP+ reductase and NADPH protochlorophyllide oxidoreductase B, have relatively low level of transcripts, and their reduction is not as dramatic as others.

Cluster 8 was also analyzed. The expression of this group of genes shows a dramatic increase towards senescence. Detailed examination of this cluster revealed 8 genes involved in senescence. Other senescence genes also increased their transcription level during late development, however, those changes were not as dramatic as the eight genes identified in cluster 8. These genes were found in cluster 2.

#### **4. Function Characterization of Global Gene Expression Pattern**

Cluster analysis also identifies co-regulated genes, and organizes the samples or array experiments according to their overall expression patterns. In order to validate the expression data, cluster analysis was performed on 6,626 genes with an expression level above background (average difference greater or equal 25) in any of the samples. All data were normalized to their median, organized into a SOM, and into a hierarchical cluster using Cluster program (Eisen et al. 1998).

According to the similarity of the global expression patterns of each sample, samples form three major clusters: a cluster of leaf samples, a cluster of supporting axis, including root, inflorescence stem and seedling samples, and a cluster of the reproductive organ samples, including samples of flowers, siliques, and inflorescences (including flowers and siliques). Similarly, genes also organized into several major classes according to their expression levels: organ-differentially expressed genes were easily highlighted.

It is worth noting that sample/experimental variations also contributed to the clusters. For example, the leaf gene expression data were produced from 2 independent experiments.

One set of the leaf materials was collected in the morning at approximately 10 o'clock, and the other set was collected in the afternoon around 3 o'clock in the afternoon. The circadian regulated gene expression contributed greatly to form two sample clusters. These circadian regulated genes matched the genes described in Hammer et al. (2000).

## 5 **5. Regulatory Sequences**

To elucidate the regulatory elements of co-regulated genes, AlignACE was employed (Hughes et al., 2000). A total of 49 promoters were found to share a few potential and known *cis*-acting elements. Among these *cis*-acting elements identified from the ribosomal promoters, the telo-box motif (AAACCCTA) was observed in 41 of these ribosomal promoters. Telo-  
10 boxes have been found in many *Arabidopsis* ribosomal genes and in eEF1A (Tremousaygue et al., 1999). This telo-box binds a protein related to Pura conserved nuclear protein that has been implicated in the control of gene transcription and DNA replication (Safak et al., 1999). Another motif identified in the ribosomal promoter regions was the Dof binding site (AAAG). The Dof binding site has been shown in the promoters of a diverse set of plant genes,  
15 suggesting various roles of Dof proteins in plants (Yanagisawa and Schmidt, 1999), including carbon metabolism (Yanagisawa, 2000). Additional motifs observed include a pollen specific motif (AGAAA) and a RAV1 binding motif (Kagaya et al., 1999).

The promoter regions from leaf-specific genes were also analyzed by AlignAce software to discover putative *cis* elements. Those that were found include a GATA box and a  
20 light regulatory element "ACGTGGCA". These elements are known to be necessary for light induced genes. A putative element that did not contain a known binding site was "TGGTTCGGACC" (SEQ ID NO:586). This element was located in 16 of the promoters analyzed.

A global gene expression pattern composed of the transcription profiles of 8,100 genes  
25 in 20 samples collected from different organs during *Arabidopsis* development was identified. By 166,000 gene expression measurements, the mRNA populations in different organs during *Arabidopsis* development were characterized. In particular, constitutively expressed genes and organ-differentially expressed genes were identified.

The accuracy of the microarray data was validated by two measures. First, the  
30 microarray results were repeatable. By comparing 15 pair of independently prepared labeled

samples, less than 0.2% of the false positive rate was observed. The false positives occurred randomly among the genes with a low expression level. Second, expression levels measured by the oligonucleotide array correlated well with data from previous gene expression analysis and measurement from other technologies, such as RT-PCR.

5 Identification of constitutively and organ-differentially expressed genes is important to isolate constitutive or organ/tissue specific promoters. Here, it is demonstrated that the microarray technology can be used for large scale screening of these promoters, especially at the genome level. Moreover, genes that are co-regulated can be analyzed to identify the regulatory elements. In this study, constitutive and organ-specific genes were identified  
10 through the screening of 8,100 genes, but also regulatory elements, such as telo-box, Dof binding site, as well as other motifs, which are important for the constitutive expression of the ribosomal proteins. By a similar approach, organ- or tissue-specific gene promoter elements, and various treatment-induced gene promoter elements, have been identified. Such results not only facilitate the dissection of the regulatory pathway, but also provide an opportunity in  
15 genetic engineering of metabolic pathways. Methods such as chimeraplasty (Zhu et al. 1999, 2000) can be used to precisely modify these regions and thus regulate a group of genes of interest.

Identification of co-regulated genes is the first step towards understanding of the regulation of a gene expression network, and assigning function to new genes. Among the  
20 8,100 genes analyzed, approximately 3,100 genes do not have significant homology to known genes. Functional characterization of these genes becomes the challenge for the *Arabidopsis* genomics. A straightforward approach can be used to assign gene function: mutant lines or treated biological samples and their controls can be transcriptionally profiled. By comparing alterations in the expression of the novel genes, potential function can be assigned. The  
25 functions can be further confirmed by reverse genetics. Alternatively, genes with unknown function in the identified co-regulated gene clusters can be computationally analyzed by support vector machines (SVMs; Brown et al. 2000).

Similar experiments were conducted for root at least 3 hours after exposure to stress, e.g., salt, mannitol or cold (Tables 9-10). Twenty-five root-specific promoters were  
30 downregulated and 8 were upregulated in response to salt stress, 21 were downregulated and

17 were upregulated in response to mannitol, and 22 were downregulated and 7 were upregulated in response to cold. Ten promoters did not respond to any of the stresses.

5    **Example 3:**     Further Analysis of Constitutively Expressed Genes

          A standard curve of 50, 10, 2, 0.4, and 0.08 ng total RNA was generated for each primer/probe set tested. In this case, the 50 ng sample yielded a  $C_t$  value of 24.5 and the 10 ng sample yields a  $C_t$  value of 26.7. The  $C_t$  value is defined as the threshold cycle whereby amplification occurs at an exponential rate. A low  $C_t$  value correlates with high gene  
10    expression. The threshold is determined empirically from the standard curve. By raising or lowering the threshold, the data set is maximized to represent optimal exponential amplification. A correlation coefficient ( $R^2$  of the best-fit line from the standard curve) greater than 99% and a slope of  $-3.3$  (most efficient amplification) is ideal. For accurate repeatable results, the previous criteria must be met and the unknowns must fall within the range of the  
15    curve. The expression levels of the unknown can be interpolated from the unknown  $C_t$  values using the standard curve.

          TaqMan chemistry employs three gene-specific oligonucleotides for the detection of nucleic acids. Two of the oligonucleotides are primers used for the amplification of the molecule and the third oligonucleotide is a probe that is labeled with a 5' fluorescent reporter  
20    dye (6-FAM) and a 3' quencher dye (TAMRA). During PCR amplification, elongation proceeds once the DNA polymerase binds to the primer. As it polymerizes in the 5' to 3' direction, the polymerase encounters the quenched probe. The 5' to 3' exonuclease activity of the polymerase allows it to degrade the probe in its path, thereby releasing the 5' reporter dye. The thermocycler is equipped with a detection system to measure the fluorescence from the  
25    released reporter dye. Since fluorescence increases with amplification of the molecule, fluorescence can be directly related to the amount of molecules in the starting sample. The primers that were employed for one set were: TRX3T 5' 6-FAM agacttcactgcaacatggtgccac TAMRA 3' (SEQ ID NO:587); TRX3F 5' gtgtggaaatgacacagattgtga3' (SEQ ID NO:588), and TRX3R 5'agacgggtgcaatgaaacg3' (SEQ ID NO:589); and for the other set were: APX3 T 5' 6-  
30    FAM cgcgacaagaactgtgctcctatcatg TAMRA 3' (SEQ ID NO:590),

APX3 F 5'gccgtgagctccgttctct3' (SEQ ID NO:591); and APX3 R 5'tcgtgccatgccaatcg3' (SEQ ID NO:592). TaqMan chemistries were used with the ABI Prism 7700 Sequence system for relative quantitation of nucleic acid.

To find a gene whose expression is constitutive, the gene expression data obtained from the *Arabidopsis* GeneChip™ was analyzed. Three sets of data were analyzed (Table 4). Part A represents expression data for 2 genes from wild-type plants infected or not infected with *Pseudomonas syringae* pv. *maculicola* strain ES4326 at 30 hours post-inoculation. Part B represents expression data from wild-type *Arabidopsis* plants infected or not infected with 5 different viruses at 1 and 4 days after inoculation, while part C represents expression data for 2 genes in 9 different tissue types.

Table 4

A:

PLANTS	TRX3	APX3
Columbia infected	2481	484
Columbia mock	2362	495

B:

DAYS	GENE	Mock	TVCV	ORMV	TRV	CMV	TuMV
1	TRX3	2020	1991	1738	2006	1833	1867
1	APX3	711	557	717	755	658	4 2 6
4	TRX3	1753	1978	1377	2249	1918	1928
4	APX3	759	674	428	551	741	434

5

C:

	TRX3	APX3
4 day seed	1282	488
2 week root	1467	435
Adult root	1857	320
2 week leaf	1233	771
Adult leaf	1483	857
Senescing leaf	1312	805
Flowers	694	513
Inflorescence	691	461
Immature siliques	614	508

After analyzing the data, 2 candidate genes were identified, thioredoxin (TRX3; Genbank Accession No. U35640) and ascorbate peroxidase (APX3; Genbank Accession No. U69138), whose expression did not vary more than 2-fold between the treatments in all experiments (except in flowers, inflorescence and siliques for TRX3). These genes also met the criteria of not having significant sequence similarity to other *Arabidopsis* genes.

Probe and primer sets were prepared for ubiquitin 5 (UBQ5), PR1 (a pathogenesis related gene whose expression is induced upon infection), TRX3 and APX3. TaqMan was used to quantify relative expression levels of these genes in *Arabidopsis* mutants and in uninfected and *P. syringae* infected plants. Table 5 shows that the PR1 expression increased rapidly upon infection. TRX3 and APX3 expression levels did not change as much as UBQ5, a commonly used gene for normalization.

Table 5. Gene expression in *Arabidopsis* infected with *P. syringae* at 34 hours post inoculation. Measured by TaqMan.

PLANTS	PR1	UBQ5	TRX3	APX3
Columbia infected	10	15	1.2	1.4
Columbia Mock	.0033	2.7	.62	1.4
Pad4 mutant infected	4.6	2.0	1.2	1.4
Pad4 mutant Mock	.00027	.79	1.1	2

Additionally, *Arabidopsis* plants were cold treated for 48 hours and the gene expression of these plants versus plants left at room temperature measured. There was no significant gene expression difference for PR1, TRX3, or APX3 (Table 6).



Table 6

	Room temperature plants	Cold-treated plants
PR1	2.6	3.2
TRX3	2.0	2.4
APX3	2.1	2.8

In summary, gene-chip data was employed to find genes whose expression is constitutive in several *Arabidopsis* mutants, in infected plants, and throughout different tissues.

5 TRX3 and APX3 expression levels varied less than UBQ5 in a comparison between infected and uninfected plants. TRX3 and APX3 gene expression was not significantly affected by cold-stress. Thus, TRX3 and APX3 are candidates for normalization when determining unknown gene expression levels in plants such as *Arabidopsis* or using quantitative PCR or other gene expression measurement assays. Likewise, the plant kingdom orthologs of these  
10 genes in dicots and monocots can be used for the same normalization standards for plants unrelated to *Arabidopsis*.

Moreover, unlike actin and ubiquitin (actin mediates cellular division and cycling and the ubiquitin pathway is activated upon stress, all of which may result in changes in gene expression), which belong to gene families to which probes can cross-hybridize, TRX3 and  
15 APX3 genes do not have significant similarity to genes in the *Arabidopsis* genome database, and the respective primer/probe sets described herein did not significantly cross-hybridize with other genes in the *Arabidopsis* genome database. Additionally, the promoters for these genes may be useful for constitutive gene expression.

#### 20 **Example 4:**     Construction of Binary Promoter::Reporter Plasmids

To construct a binary promoter:: reporter plasmid for *Arabidopsis* transformation a vector containing a promoter of interest (i.e., the DNA sequence 5' of the initiation codon for the gene of interest) was used, which resulted from recombination in a BP reaction between a PCR product using the promoter of interest as a template and pDONRneo. The  
25 regulatory/promoter sequence was fused to the GUS reporter gene (Jefferson et al, 1987) by recombination using GATEWAY™ Technology according to manufacturers protocol as

described in the Instruction Manual (GATEWAY™ Cloning Technology, GIBCO BRL, Rockville, MD <http://www.lifetech.com/>). Briefly, the promoter fragment in the vector is recombined via the LR reaction with a binary *Agrobacterium* destination vector containing the GUS coding region with an intron that has an *attR* site 5' to the GUS reporter (pNOV2374).

- 5 The orientation of the inserted fragment was maintained by the *att* sequences and the final construct was verified by sequencing. The construct was then transformed into *Agrobacterium tumefaciens* strains by electroporation.

- pNOV2374 is a binary vector with a VS1 origin of replication, a copy of the *Agrobacterium virG* gene in the backbone and a Basta resistance selectable marker cassette  
10 between the left and right border sequences of the T-DNA (SEQ ID NO:581).

- The Basta selectable marker cassette comprises the *Agrobacterium tumefaciens* manopine synthase promoter (AtMas et al., 1983) operably linked to the gene encoding Basta resistance (denoted here as "BAR", phosphinothricin acetyl transferase, White et al, 1990) and the 35S terminator. The AtMas promoter, BAR coding sequence and 35S terminator are  
15 located at nt 4211 to 4679, nt 4680 to 5228, and nt 5263 to 5488, respectively, of pNOV2374. The vector contains GATEWAY™ recombination components which were introduced into the binary vector backbone by ligating a blunt-ended cassette containing *attR* sites, *ccdB* and chloramphenicol resistance marker using the GATEWAY™ Vector Conversion System (LifeTechnologies, [www.lifetech.com](http://www.lifetech.com)). The GATEWAY™ cassette is located between nt  
20 126 and 1818 of pNOV2374. The promoter cassettes are inserted through an LR recombination reaction whereby the DNA sequence of pNOV2374 between nt 126 and nt 1818 are removed and replaced with the promoter of interest flanked by *att* sequences. The recombination results in the promoter sequence fused to the GUS reporter gene with intron (GIG) sequence. The GIG gene contains the ST-LS1 intron from *Solanum tuberosum* at nt  
25 385 to nt 576 of GUS (SEQ ID NO:582) (obtained from Dr. Stanton Gelvin, and described in Narasimhulu et al, 1996). Shown below in Table 7 are the orientations of the selectable marker and promoter-reporter cassettes in the binary vector constructs.

Table 7

	RB--AC9 promoter fragment (SEQ ID NO: 548)+GIG gene + nos -- x --LB
	RB--AC11 promoter fragment (SEQ ID NO: 550)+GIG gene + nos -- x --LB
5	RB--AC12 promoter fragment (SEQ ID NO: 551)+GIG gene + nos -- x --LB
	RB--AC13 promoter fragment (SEQ ID NO: 552)+GIG gene + nos -- x --LB
	RB--AC14 promoter fragment (SEQ ID NO: 553)+GIG gene + nos -- x --LB
	RB--AC16 promoter fragment (SEQ ID NO: 555)+GIG gene + nos -- x --LB
	RB--AC19 promoter fragment (SEQ ID NO: 556)+GIG gene + nos -- x --LB
10	RB--AC20 promoter fragment (SEQ ID NO: 557)+GIG gene + nos -- x --LB
	RB--AC21 promoter fragment (SEQ ID NO: 558)+GIG gene + nos -- x --LB
	RB--AC23 promoter fragment (SEQ ID NO: 560)+GIG gene + nos -- x --LB
	RB--AC31 promoter fragment (SEQ ID NO: 565)+GIG gene + nos -- x --LB
	RB--AC32 promoter fragment (SEQ ID NO: 566)+GIG gene + nos -- x --LB
15	RB--AC34 promoter fragment (SEQ ID NO: 567)+GIG gene + nos -- x --LB
	RB--AC35 promoter fragment (SEQ ID NO: 568)+GIG gene + nos -- x --LB
	RB--AC40 promoter fragment (SEQ ID NO: 571)+GIG gene + nos -- x --LB
	RB--AC42 promoter fragment (SEQ ID NO: 572)+GIG gene + nos -- x --LB
	RB--AC44 promoter fragment (SEQ ID NO: 573)+GIG gene + nos -- x --LB
20	RB--AC46 promoter fragment (SEQ ID NO: 575)+GIG gene + nos -- x --LB
	RB--AC47 promoter fragment (SEQ ID NO: 576)+GIG gene + nos -- x --LB
	RB--1B-1 promoter fragment (SEQ ID NO: 578)+GIG gene + nos -- x --LB
	RB--1G-2 promoter fragment (SEQ ID NO: 579)+GIG gene + nos -- x --LB
	RB--1AMix1-C promoter fragment (SEQ ID NO: 577)+GIG gene + nos -- x --LB
25	RB--AR1 promoter fragment (SEQ ID NO: 536)+GIG gene + nos -- x --LB
	RB--AR2 promoter fragment (SEQ ID NO: 537)+GIG gene + nos -- x --LB
	RB--AR6 promoter fragment (SEQ ID NO: 539)+GIG gene + nos -- x --LB
	RB--AR8 promoter fragment (SEQ ID NO: 540)+GIG gene + nos -- x --LB
	RB--AR9 promoter fragment (SEQ ID NO: 541)+GIG gene + nos -- x --LB
30	RB--AR10 promoter fragment (SEQ ID NO: 542)+GIG gene + nos -- x --LB

x = AtMas + BAR + 35S ter

For comparison of promoter activity an additional construct was produced with the known Arabidopsis ubiquitin 3 (Ubq3(At), (Callis et al., 1990) promoter plus intron operatively linked to the GIG gene and the *nos* promoter. The artificial sequence of the *Arabidopsis* Ubiquitin3 promoter plus intron (Ubq3 (At)) is provided in SEQ ID NO:583. Thus, the orientation of the selectable marker and promoter-reporter cassette in the binary vector construct was RB-- Ubq3(At) promoter with intron fragment+GIG gene + nos --AtMas + BAR + 35S ter --LB

**Example 5: *In vitro* Promoter Assays and *Arabidopsis* Transformation Plant preparation and growth**

*Arabidopsis* seeds are sown on moistened Fafard Germinating Mix at a density of 9 seeds per 4" square pot, placed in a flat, covered with a plastic dome to retain moisture and moved to a growth chamber. Following germination the dome is removed and plants are grown for 3-5 weeks under short days (8 hrs light) to encourage vegetative growth and production of large plants with many flowers. Flowering is induced by providing long days (16 hrs. light) for 2-3 weeks, at which time plants are ready for dip inoculation into *Agrobacterium* to generate transgenic plants.

**Agrobacterium transformation, culture growth and preparation for plant infiltration**

The binary promoter::reporter plasmids are introduced into *Agrobacteria* by electroporation. The binary plasmid confers spectinomycin resistance to the bacteria allowing cells containing the plasmid to be selected by growth of colonies on plates of LB + spectinomycin (50 mg/L). Presence of the correct promoter::GUS plasmid is confirmed by sequence analysis of the plasmid DNA isolated from the bacteria.

Two days prior to plant transformation 5 mL cultures of LB + spectinomycin (50 mg/L) are inoculated with the *Agrobacterium* strain containing the binary promoter::GUS plasmid and incubated at 30°C for about 24 hours. Each 5 mL culture is then transferred to 500 mL of LB + spectinomycin (50 mg/L) and incubated for about 24 hours at 30°C. Each 500 mL culture is transferred to a centrifuge bottle and centrifuged at 5000 rpm for 10 minutes in a Sorvall Centrifuge. The supernatant is removed and the pelleted *Agrobacterium* cells are retained. The *Agrobacterium* cells are resuspended in 500 mL of modified Infiltration Media

(IM+MOD: 50g/L sucrose, 10 mM MgCl, 10 uM benzylaminopurine ) to which 50 ul of Silwet L-77 (Dupont) has been added.

#### Plant transformation by dip infiltration

Resuspended cells are poured into 1L tri-pour beakers. Flowering plants are inverted  
5 into the culture, making sure all inflorescences are covered with the bacteria. The beakers are gently agitated for 30 seconds, keeping all inflorescence tissue submerged. Plants are returned to growth chamber following dip inoculation of the *Agrobacterium*. A second dip may be performed 5 days later to increase transformation frequency. Seeds are harvested ~4 to 6 weeks after transformation.

#### 10 Selection of transgenic *Arabidopsis*

Seeds from transformed *Arabidopsis* plants are sown on moistened Fafard Germinating Mix in a flat, covered with a dome to retain moisture and placed in a growth chamber. Following germination seedlings are sprayed with the herbicide BASTA. Transgenic plants are BASTA resistant due to the presence of the BAR gene in the binary promoter::GUS plasmid.

#### 15 Promoter Assays

Promoter activity is evaluated qualitatively and quantitatively using histochemical and florescence assays for expression of the  $\beta$ -glucuronidase (GUS) enzyme.

#### Histochemical $\beta$ -glucuronidase (GUS) assay

For qualitative evaluation of promoter activity, various *Arabidopsis* tissues and organs  
20 are used in GUS histochemical assays. Either whole organs or pieces of tissue are dipped into GUS staining solution. GUS staining solution contains 1 mM 5-bromo-4-chloro-3-indolyl glucuronide (X-Gluc, Duchefa, 20 mM stock in DMSO), 100 mM Na-phosphate buffer pH 7.0, 10 mM EDTA pH 8.0, and 0.1% Triton X100. Tissue samples are incubated at 37°C for 1-16 hours. If necessary samples can be cleared with several washes of 70% EtOH to remove  
25 chlorophyll. Following staining tissues are viewed under a light microscope to evaluate the blue staining showing the GUS expression pattern.

#### $\beta$ -glucuronidase (GUS) florescence assay

For quantitative analysis of promoter activity in various *Arabidopsis* tissues and organs, GUS expression is measured fluorometrically. Tissue samples are harvested and ground in ice  
30 cold GUS extraction buffer (50 mM Na<sub>2</sub>HPO<sub>4</sub> pH 7.0, 5 mM DTT, 1 mM Na<sub>2</sub>EDTA, 0.1% Triton X100, 0.1% sarcosyl). Ground samples are spun in a microfuge at 10,000 rpm for 15

minutes at 4 °C. Following centrifugation the supernatant is removed for GUS assay and for protein concentration determination.

To measure GUS activity the plant extract is assayed in GUS assay buffer (50 mM Na<sub>2</sub>HPO<sub>4</sub> pH 7.0, 5 mM DTT, 1 mM Na<sub>2</sub>EDTA, 0.1% TritonX100, 0.1% sarcosyl, 1 mM 4-Methylumbelliferyl-beta-D-glucuronic acid dihydrate (MUG)), prewarmed to 37°C. Reactions are incubated and 100 uL aliquots are removed at 10 minute intervals for 30 minutes to stop the reaction by adding to tubes containing 900 uL of 2% Na<sub>2</sub>CO<sub>3</sub>. The stopped reactions are then read on a Tecan Spectrofluorometer at 365 nm excitation and 455 emission wavelengths. Protein concentrations are determined using the BCA assay following manufacturers protocol. GUS activity is expressed as relative fluorometric units (RFU)/mg protein.

**Example 6: Determination of the minimal promoter fragment**

The full-length promoter sequence as given in SEQ ID Nos: 536-579, more preferably in any one of SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter orthologs thereof is fused to the  $\beta$ -glucuronidase (GUS) gene at the native ATG to obtain a chimeric gene cloned into plasmid DNA. The plasmid DNA is then digested with restriction enzymes to release a fragment comprising the full-length promoter sequence and the GUS gene, which is then used to construct the binary vector. This binary vector is transformed into *Agrobacterium tumefaciens*, which is in turn used to transform *Arabidopsis* plants (for further details of the binary vector construction see above example 4)

The above plasmid can also be used to form a series of 5' end deletion mutants having increasingly shorter promoter fragments fused to the GUS gene at the native ATG. Various restriction enzymes are used to digest the plasmid DNA to obtain the binary vectors with different lengths of promoter fragments. In particular, a binary vector 1 is constructed with a 1,900-bp long promoter fragment; a binary vector 2 is constructed with a 1,300-bp long promoter fragment; a binary vector 3 is constructed with a 1000-bp long promoter fragment; a binary vector 4 is constructed with a 800-bp long promoter fragment; a binary vector 5 is constructed with a 700-bp long promoter fragment; a binary vector 6 is constructed with a 600-bp long promoter fragment; a binary vector 6 is constructed with a 500-bp long promoter

fragment; and a binary vector 7 is constructed with a 100-bp long promoter fragment. Like the binary vector comprising the full-length promoter fragment, these 5' end deletion mutants are also transformed into *Agrobacterium tumefaciens* and, in turn, *Arabidopsis* plants (for further details of *Arabidopsis* transformation and promoter assay procedures see example 5 above).

5        The presence of the correct hybrid construct in the transgenic lines is confirmed by PCR amplification.

By using the above protocol it can be determined, which portion of the promoter sequences given in SEQ ID Nos: 536-579, more preferably in any one of SEQ ID Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter  
10 orthologs thereof is required for gene expression.

Minimal promoter fragments having lengths substantially less than the full-length promoter can therefore be operatively linked to coding sequences to form smaller constructs than can be formed using the full-length promoter. As noted earlier, shorter DNA fragments are often more amenable to manipulation than longer fragments. The chimeric gene constructs  
15 thus formed can then be transformed into hosts such as crop plants to enable at-will regulation of coding sequences in the hosts.

#### **Example 7:      Determination of Promoter Motifs**

While a deletion analysis characterizes regions in a promoter that are required overall  
20 for its regulation, linker-scanning mutagenesis allows for the identification of short defined motifs whose mutation alters the promoter activity. Accordingly, a set of linker-scanning mutant promoters fused to the coding sequence of the GUS reporter gene are constructed. Each of them contains a 8-10-bp mutation located between defined positions and included in a promoter fragment as given in SEQ ID Nos: 536-579, more preferably to any one of SEQ ID  
25 Nos: 536; 537; 539-542; 548; 550-553; 555-558; 560; 565-568; 571-576, 578 and 579, or the promoter orthologs thereof.

Each construct is transformed into *Arabidopsis* and GUS activity is assayed for 19 to  
30 independent transgenic lines. The presence of the correct hybrid construct in transgenic lines is confirmed by PCR amplification of all lines containing the mutant constructs and by random sampling of lines containing the other constructs. Amplified fragments are digested

with restriction enzyme (e.g. XbaI) and separated on high resolution agarose gels to distinguish between the different mutant constructs. The effect of each mutation on promoter activity is compared to an equivalent number of transgenic lines containing the unmutated construct. Two repetitions resulting from independent plating of seeds are carried out in every case.

The sequences mutated in the linker-scanning constructs, in particular those that showed marked differences from the control construct, are then examined more closely.

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All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to

25 additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

**Appendix:**

Table 8 provides a description of the corresponding genes for the *Arabidopsis* sequences which are expressed in a root-specific manner.

5 Table 8:

Accession #	Affy #	Description
A71588.1	14015_s_at	pir T10626 reticuline oxidase homolog F21C20.190 - <i>Arabidopsis thaliana</i> >gil5262224 embl CAB45850.1  (AL080254) reticuline oxidase-like protein [ <i>Arabidopsis thaliana</i> ] >gil7268880 embl CAB79084.1  (AL161553) reticuline oxidase-like protein [ <i>Arabidopsis thaliana</i> ]
A71596.1	14016_s_at	gblAAD25763.1 AC007060_21 (AC007060) Strong similarity to F19I3.2 gil3033375 putative berberine bridge enzyme from <i>Arabidopsis thaliana</i> BAC gblAC004238.
A71597.1	12079_s_at	"gblAAD25757.1 AC007060_15 (AC007060) Strong similarity to F19I3.2 gil3033375 putative berberine bridge enzyme from <i>Arabidopsis thaliana</i> BAC gblAC004238. ESTs gblF19886, gblZ30784 and gblZ30785 come from this gene"
AB023448.2	12332_s_at	dbj BAA82824.1  (AB023462) basic endochitinase [ <i>Arabidopsis thaliana</i> ]
AC001645.19	15965_at	gblAAC08601.1  (AF054906) myrosinase-binding protein homolog [ <i>Arabidopsis thaliana</i> ]
AC001645.47	15996_at	gblAAB63635.1  (AC001645) jasmonate inducible protein isolog [ <i>Arabidopsis thaliana</i> ]
AC001645.50	15981_at	gblAAB63635.1  (AC001645) jasmonate inducible protein isolog [ <i>Arabidopsis thaliana</i> ]
AC002333.199	13552_at	gblAAB64044.1  (AC002333) putative endochitinase [ <i>Arabidopsis thaliana</i> ]
AC002333.210	13154_s_at	sp Q06209 CHI4_BRANA BASIC ENDOCHITINASE CHB4 PRECURSOR >gil7435353 pir S25311 chitinase (EC 3.2.1.14) precursor - rape >gil17799 embl CAA43708.1  (X61488) chitinase [ <i>Brassica napus</i> ]

Accession #	Affy #	Description
AC002391.150	17842_i_at	pir T04731 cytochrome P450 homolog F6G17.20 - Arabidopsis thaliana >gil4468803 emblCAB38204.1  (AL035601) cytochrome P450-like protein [Arabidopsis thaliana] >gil7270719 emblCAB80402.1  (AL161591) cytochrome P450-like protein [Arabidopsis thaliana]
AC003673.201	16481_s_at	pir T01626 peroxidase (EC 1.11.1.7) ATP22a - Arabidopsis thaliana >gil3004558 gblAAC09031.1  (AC003673) peroxidase (ATP22a) [Arabidopsis thaliana]
AC004005.104	19390_at	pir T00681 hypothetical protein F6E13.14 - Arabidopsis thaliana >gil3212858 gblAAC23409.1  (AC004005) unknown protein [Arabidopsis thaliana]
AC004521.114	19195_at	pir T02393 hypothetical protein F4I1.19 - Arabidopsis thaliana >gil3128201 gblAAC16105.1  (AC004521) unknown protein [Arabidopsis thaliana]
AC004521.119	20608_s_at	pir T02393 hypothetical protein F4I1.19 - Arabidopsis thaliana >gil3128201 gblAAC16105.1  (AC004521) unknown protein [Arabidopsis thaliana]
AC004683.79	16461_i_at	sp P24102 PERE_ARATH BASIC PEROXIDASE E PRECURSOR >gil81653 pir JU0458 peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana >gil166807 gblAAA32842.1  (M58381) peroxidase [Arabidopsis thaliana]
AC004684.165	17907_s_at	pir T02541 hypothetical protein F13M22.25 - Arabidopsis thaliana >gil3236257 gblAAC23645.1  (AC004684) unknown protein [Arabidopsis thaliana]
AC005310.6	17697_at	pir T02675 hypothetical protein F19D11.2 - Arabidopsis thaliana >gil3510249 gblAAC33493.1  (AC005310) unknown protein [Arabidopsis thaliana]
AC005560.136	16016_at	pir G71401 probable major latex protein - Arabidopsis thaliana >gil2244762 emblCAB10185.1  (Z97335) major latex protein like [Arabidopsis thaliana] >gil7268111 emblCAB78448.1  (AL161538) major latex protein like [Arabidopsis thaliana]
AC005560.147	12758_at	pir G71401 probable major latex protein - Arabidopsis thaliana >gil2244762 emblCAB10185.1  (Z97335) major latex protein like [Arabidopsis thaliana] >gil7268111 emblCAB78448.1  (AL161538) major latex protein like [Arabidopsis thaliana]

Accession #	Affy #	Description
AC005967.50	17864_at	emblCAA18195.1l (AL022198) putative protein [Arabidopsis thaliana] >gil7270000 emblCAB79816.1l (AL161578) putative protein [Arabidopsis thaliana]
AC006216.22	14050_at	gblAAD12680.1l (AC006216) Similar to gil3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gblAC004747
AC006216.26	18571_at	"gblAAD12679.1l (AC006216) Similar to gil3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gblAC004747. ESTs gblT44298, gblT42447, gblR64761 and gblI100206 come from this gene"
AC006577.16	12778_r_at	"gblAAD25772.1l AC006577_8 (AC006577) Belongs to the PF100657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gblT44453, gblT04815, gblT45993, gblR30138, gblAI099570 and gblT22281 come from this gene. [Arabidopsis thaliana]"
AC006587.164	15859_at	gblAAD21491.1l (AC006587) unknown protein [Arabidopsis thaliana]
AC007060.34	19840_s_at	gblAAD25758.1l AC007060_16 (AC007060) Strong similarity to F19I3.2 gil3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gblAC004238
AC007135.23	20176_at	gblAAD41993.1l AC006233_16 (AC006233) unknown protein [Arabidopsis thaliana]
AC007584.48	20194_at	gblAAF20251.1l AC015450_12 (AC015450) unknown protein [Arabidopsis thaliana]
ACHI	12852_s_at	dbj BAA21873.1l (AB006068) acidic endochitinase [Arabidopsis thaliana]
AF098630.3	19118_s_at	gblAAD12259.1l (AF098631) putative cell wall-plasma membrane disconnecting CLCT protein [Arabidopsis thaliana]

Accession #	Affy #	Description
AF128395.12	20395_at	"sp P33154 PR1_ARATH PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1) >gil322557 pir  JQ1693 pathogenesis-related protein 1 precursor, 17.6K - Arabidopsis thaliana >gil166861 gblAAA32863.1  (M90508) PR-1-like protein [Arabidopsis thaliana] >gil3810599 gblAAC69381.1  (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]"
AJ133036.5	15969_s_at	sp P24101 PERC_ARATH NEUTRAL PEROXIDASE C PRECURSOR >gil81652 pir  JU0457 peroxidase (EC 1.11.1.7) C - Arabidopsis thaliana >gil166827 gblAAA32849.1  (M58380) peroxidase [Arabidopsis thaliana] >gil6522555 emblCAB61999.1  (AL132967) peroxidase [Arabidopsis thaliana] >gil742247 prf  2009327A peroxidase [Arabidopsis thaliana]
AL024486.185	16299_at	sp P42620 YQJG_ECOLI HYPOTHETICAL 37.4 KD PROTEIN IN EXUR-TDCC INTERGENIC REGION (O328) >gil7465984 pir  C65099 hypothetical 37.4 kD protein in exuR-tdcC intergenic region - Escherichia coli (strain K-12) >gil606043 gblAAA57906.1  (U18997) ORF_o328 [Escherichia coli] >gil1789489 gblAAC76137.1  (AE000392) putative transferase [Escherichia coli]
AL035538.245	16514_at	pir  T05635 hypothetical protein F20D10.200 - Arabidopsis thaliana >gil4467114 emblCAB37548.1  (AL035538) putative protein [Arabidopsis thaliana] >gil7270791 emblCAB80473.1  (AL161592) putative protein [Arabidopsis thaliana]
AL049500.57	16914_s_at	sp P50700 OSL3_ARATH OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gil1362001 pir  S57524 osmotin precursor - Arabidopsis thaliana >gil887390 emblCAA61411.1  (X89008) osmotin [Arabidopsis thaliana]
AL049638.193	20029_at	pir  T06615 hypothetical protein F16J13.150 - Arabidopsis thaliana >gil4586113 emblCAB40949.1  (AL049638) putative DNA-binding protein [Arabidopsis thaliana] >gil7267909 emblCAB78251.1  (AL161533) putative DNA-binding protein [Arabidopsis thaliana]

Accession #	Affy #	Description
AL049730.104	18983_s_at	"pirllS42552 proline-rich protein - rape >gil545029 gblAAC60566.1  (S68113) proline-rich SAC51 [Brassica napus=oilseed rape, pods, Peptide, 147 aa]"
AL080253.32	19415_at	gblAAF08575.1 AC011623_8 (AC011623) unknown protein [Arabidopsis thaliana]
AL080282.74	18597_at	pirllT10624 reticuline oxidase homolog F21C20.170 - Arabidopsis thaliana >gil5262222 emblCAB45848.1  (AL080254) reticuline oxidase-like protein [Arabidopsis thaliana] >gil7268878 emblCAB79082.1  (AL161553) reticuline oxidase-like protein [Arabidopsis thaliana]
ATAJ2596	16085_s_at	emblCAB16787.1  (Z99707) patatin-like protein [Arabidopsis thaliana] >gil7270656 emblCAB80373.1  (AL161590) patatin-like protein [Arabidopsis thaliana]
ATHORF	16649_s_at	gblAAF16563.1 AC012563_16 (AC012563) putative S- adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]
ATPIN2	12932_s_at	gblAAD04377.1  (AF089085) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]
ATU10034	15120_s_at	sp Q42521 DCE1_ARATH GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gil497979 gblAAA93132.1  (U10034) glutamate decarboxylase [Arabidopsis thaliana]
ATU57320	15137_s_at	gblAAB47973.1  (U57320) blue copper-binding protein II [Arabidopsis thaliana]
ATU62330	15623_f_at	dbj BAA24282.1  (AB000094) inorganic phosphate transporter [Arabidopsis thaliana]
BCHI	13211_s_at	dbj BAA82824.1  (AB023462) basic endochitinase [Arabidopsis thaliana]
CAFFEROYLCO A - METHYLTRANS	13215_s_at	gblAAA62426.1  (L40031) S-adenosyl-L- methionine:trans-caffeoyl-Coenzyme A 3-O- methyltransferase [Arabidopsis thaliana]
NOVARTIS51	14170_at	gblAAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
U72155.2	15954_at	gblAAB64244.1  (U72155) beta-glucosidase [Arabidopsis thaliana]

Accession #	Affy #	Description
U81294.2	20422_g_at	gb AAD00509.1  (U81294) germin-like protein [Arabidopsis thaliana]
X67421.3	16489_at	pir S53012 root-specific protein RCc3 - rice >gil786132 gb AAA65513.1  (L27208) RCc3 [Oryza sativa]
X74514.2	20239_g_at	dbj BAA89048.1  (AB029310) beta-fructofuranosidase [Arabidopsis thaliana]
X78586.2	16048_at	pir S51480 drought-induced protein Dr4 - Arabidopsis thaliana >gil469114 embl CAA55323.1  (X78586) Dr4 [Arabidopsis thaliana]
X98319.2	16971_s_at	embl CAA66963.1  (X98319) peroxidase [Arabidopsis thaliana] >gil1429217 embl CAA67311.1  (X98775) peroxidase ATP12a [Arabidopsis thaliana] >gil6714469 gb AAF26155.1 AC008261_12 (AC008261) putative peroxidase [Arabidopsis thaliana]
X98320.2	18312_s_at	gb AAF63027.1 AF244924_1 (AF244924) peroxidase prx15 precursor [Spinacia oleracea]
X98321.2	19595_s_at	gb AAB71452.1  (AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb X98321). [Arabidopsis thaliana] >gil2738254 gb AAB94661.1  (U97684) peroxidase precursor [Arabidopsis thaliana]
X98322.2	17942_s_at	gb AAF03466.1 AC009327_5 (AC009327) putative peroxidase [Arabidopsis thaliana]
X98808.1	15985_at	embl CAA67340.1  (X98808) peroxidase ATP3a [Arabidopsis thaliana]
X98855.2	16028_at	pir T01626 peroxidase (EC 1.11.1.7) ATP22a - Arabidopsis thaliana >gil3004558 gb AAC09031.1  (AC003673) peroxidase (ATP22a) [Arabidopsis thaliana]
Y11788.1	18946_at	embl CAA72484.1  (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
Z97338.321	16045_s_at	pir E71418 hypothetical protein - Arabidopsis thaliana >gil2244897 embl CAB10319.1  (Z97338) HSR201 like protein [Arabidopsis thaliana] >gil7268287 embl CAB78582.1  (AL161541) HSR201 like protein [Arabidopsis thaliana]



Accession #	Affy #	Description
Z97340.345	17485_s_at	"sp P52407 E13B_HEVBR GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gil2129912 pir S65077 1,3-beta-glucanase (EC 3.2.1.-) precursor - Para rubber tree >gil1184668 gblAAA87456.1  (U22147) beta-1,3-glucanase [Hevea brasiliensis]"
Z97344.151	19886_at	gblAAC61811.1  (AC004667) putative AT-hook DNA-binding protein [Arabidopsis thaliana]
Z99707.288	18326_s_at	emblCAB16788.1  (Z99707) patatin-like protein [Arabidopsis thaliana] >gil7270655 emblCAB80372.1  (AL161590) patatin-like protein [Arabidopsis thaliana]

Table 9 shows expression results from an acute (3 hour) response to stress, either up or down, to cold, mannitol, or salt in roots but not in leaves. Of the nine root-specific promoters shown in Table 8, one (SEQ ID NO:8) did not show a response to any of the stresses, two (SEQ ID NOs. 47 and 48) were downregulated in response to cold, mannitol and stress, four (SEQ ID NOs:4, 7, 28 and 30) were upregulated in response to at least one of the stresses and downregulated in response to at least one of the stresses, and two (SEQ ID NOs:25 and 28) were only downregulated by salt stress.

Table 9:

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Accession	Affy id	Cold Root3	Cold Root27	Man Root3	Man Root27	Salt Root3	Salt Root27
Roots							
AC006577.16	12778_r_at	-1985	-3753	-2768	-363	-4018	-1769
ATU57320	15137_s_at	-729	-219	-1304	992	-2420	141
X98808.1	15985_at	-2123	1183	-1881	-312	-2331	-343
U81294.2	20421_at	-19	2399	-1162	345	-1450	371
Z97338.321	16045_s_at	-1068	-694	-1084	124	-1425	-285
X98855.2	16028_at	-448	-691	-595	-589	-1043	-559
AC006577.16	12779_f_at	-672	-763	-636	-419	-976	-559
X78586.2	16048_at	56	603	-576	307	-881	-588
ATU62330	15623_f_at	-1274	373	-1054	141	-817	439
NOVARTIS51	14170_at	-1058	537	-654	-14	-718	16
AC005560.136	16016_at	93	643	25	628	-648	-232
AF098630.3	19118_s_at	228	422	-52	-37	-640	-117
AF128395.12	20395_at	-286	-508	-482	-115	-621	261
Z97340.345	17485_s_at	-691	-1934	-357	-592	-529	-454
AL035538.245	16514_at	200	-498	798	935	-490	-118
X98322.2	17942_s_at	-366	54	-285	4	-457	3
ATU10034	15120_s_at	-102	134	-336	-80	-456	-65
AL049730.104	18983_s_at	322	-51	-272	-167	-439	-570

Accession	Affy id	Cold Root3	Cold Root27	Man Root3	Man Root27	Salt Root3	Salt Root27
AJ133036.5	15969_s_at	-316	-619	74	-465	-400	-470
U72155.2	15954_at	52	-178	-86	-447	-388	-252
X98319.2	16971_s_at	-368	9	-291	-62	-368	-86
U81294.2	20422_g_at	-96	530	-272	43	-341	32
X67421.3	16489_at	446	200	-158	-41	-323	-357
Y11788.1	18946_at	100	146	-58	-21	-199	124
ATPIN2	12932_s_at	-172	-182	-158	-67	-170	-128
AC005310.6	17697_at	-99	18	-97	-15	-139	-23
AC007135.23	20176_at	-37	82	260	137	-120	-81
AC006587.164	15859_at	91	134	29	13	-117	-8
AC004521.114	19195_at	-410	93	-322	-36	-96	-20
X98321.2	19595_s_at	-50	-149	-66	0	-95	73
AC002333.199	13552_at	-205	-418	167	101	-89	-148
AL024486.185	16299_at	-162	-165	-76	-47	-80	-20
AC004521.119	20608_s_at	-201	96	-119	-7	-75	15
A71597.1	12079_s_at	-185	-153	79	-142	-74	-60
AC006216.26	18571_at	-46	55	23	-26	-71	10
AC006216.22	14050_at	-45	14	-23	-14	-62	-8
AL080253.32	19415_at	112	-132	107	118	-56	-108
AC004683.79	16461_i_at	-145	-621	-136	-164	-17	142
X74514.2	20239_g_at	13	213	60	-91	1	1
AL080282.74	18597_at	-251	161	-58	120	4	-24
AC002333.210	13153_r_at	-5	-186	48	-82	9	-51
X74514.2	20238_at	288	553	174	115	10	302
CAFFEROYLCOA-METHYLTRANS	13215_s_at	42	33	38	-20	12	-56
AC004005.104	19390_at	-77	0	-121	37	13	-16
ATHORF	16649_s_at	54	112	43	17	16	-8
AC003673.201	16481_s_at	-38	-106	16	-22	17	-28

Accession	Affy id	Cold Root3	Cold Root27	Man Root3	Man Root27	Salt Root3	Salt Root27
ATAJ2596	16085_s_at	128	-137	240	64	30	-47
AC002333.210	13154_s_at	-6	-511	168	-224	31	-172
AC004684.165	17907_s_at	-154	-52	-3	106	40	65
AL049638.193	20029_at	45	41	35	-42	64	-20
A71588.1	14015_s_at	-130	138	164	-23	79	-1
A71596.1	14016_s_at	-104	99	132	-15	98	1
Z99707.288	18326_s_at	150	-110	309	19	99	-75
ACHI	12852_s_at	-25	36	97	-7	114	-20
AC005560.147	12758_at	33	-822	362	357	121	146
X98320.2	18312_s_at	38	29	293	21	131	-14
AC002391.150	17843_s_at	79	170	26	15	177	1
AC005967.50	17864_at	37	133	41	-37	196	-4
AC007060.34	19840_s_at	606	1194	304	-145	286	185
BCHI	13211_s_at	99	-554	337	-242	312	-275
AC001645.19	15965_at	-323	-177	141	-437	355	-389
AB023448.2	12332_s_at	170	-704	421	-130	370	-374
AC001645.47	15996_at	-160	-167	215	-162	445	-147
AL049500.57	16914_s_at	96	-2596	366	-818	541	-1265
AC007584.48	20194_at	288	0	848	259	1016	-116

Accession	Affy id	Cold Leaf3	Cold Leaf 27	Man Leaf 3	Man Leaf 27	Salt Leaf 3	Salt Leaf 27
Leaves							
AC006577.16	12778_r_at	80	-89	92	-81	-14	-167
ATU57320	15137_s_at	158	63	53	5	-35	-79
X98808.1	15985_at	-5	-136	-11	-137	5	-93
U81294.2	20421_at	35	-8	18	81	52	-19
Z97338.321	16045_s_at	10	-8	1	2	5	-4
X98855.2	16028_at	-1	-16	-2	-13	1	-13

Accession	Affy id	Cold Leaf3	Cold Leaf 27	Man Leaf 3	Man Leaf 27	Salt Leaf 3	Salt Leaf 27
AC006577.16	12779_f_at	-83	-57	-47	-53	-34	-58
X78586.2	16048_at	69	96	149	78	36	81
ATU62330	15623_f_at	-3	8	-4	42	49	-14
NOVARTIS51	14170_at	-188	1031	-258	-311	-310	-195
AC005560.136	16016_at	1	0	7	7	4	5
AF098630.3	19118_s_at	1	-9	-6	1	-2	-5
AF128395.12	20395_at	3	1	10	3	6	-2
Z97340.345	17485_s_at	103	-619	20	-200	-54	-521
AL035538.245	16514_at	15	10	6	10	5	-2
X98322.2	17942_s_at	-1	0	-2	-2	2	-1
ATU10034	15120_s_at	10	-85	-3	-81	-3	-25
AL049730.104	18983_s_at	-6	13	0	14	-4	7
AJ133036.5	15969_s_at	4	13	12	13	25	7
U72155.2	15954_at	4	4	0	-7	4	-2
X98319.2	16971_s_at	-4	3	3	-2	1	-5
U81294.2	20422_g_at	12	0	6	9	11	-4
X67421.3	16489_at	-3	2	-5	0	-2	2
Y11788.1	18946_at	-177	-203	-175	-204	-158	285
ATPIN2	12932_s_at	-13	-1	-2	1	-3	-6
AC005310.6	17697_at	-3	2	-1	-3	0	-5
AC007135.23	20176_at	8	3	0	-1	1	-6
AC006587.164	15859_at	-51	-62	-54	-47	-56	50
AC004521.114	19195_at	-35	2	-12	1	-3	-21
X98321.2	19595_s_at	2	-4	-1	0	0	2
AC002333.199	13552_at	4	7	-1	2	1	6
AL024486.185	16299_at	-15	-139	-26	-33	-31	-35
AC004521.119	20608_s_at	-18	1	-15	-2	2	-6
A71597.1	12079_s_at	-4	-22	-5	-10	5	-7
AC006216.26	18571_at	-1	9	2	10	4	10

Accession	Affy id	Cold Leaf3	Cold Leaf 27	Man Leaf 3	Man Leaf 27	Salt Leaf 3	Salt Leaf 27
AC006216.22	14050_at	-2	-1	-3	-4	-2	2
AL080253.32	19415_at	6	0	3	0	2	6
AC004683.79	16461_i_at	26	0	8	17	14	21
X74514.2	20239_g_at	-11	84	4	-60	-55	-48
AL080282.74	18597_at	-62	284	27	36	-40	23
AC002333.210	13153_r_at	52	-23	41	35	-6	-42
X74514.2	20238_at	-9	218	0	-112	-180	-194
CAFFEROYLCOA-METHYLTRANS	13215_s_at	20	31	7	0	1	-8
AC004005.104	19390_at	8	-3	-3	1	4	-13
ATHORF	16649_s_at	47	39	9	2	-2	-8
AC003673.201	16481_s_at	3	0	0	5	1	7
ATAJ2596	16085_s_at	0	-1	-9	2	-3	1
AC002333.210	13154_s_at	74	-63	198	75	-20	-84
AC004684.165	17907_s_at	17	-29	16	25	15	-8
AL049638.193	20029_at	-4	-18	-6	-5	0	-9
A71588.1	14015_s_at	5	-7	2	-6	13	-10
A71596.1	14016_s_at	8	-3	11	-2	-1	1
Z99707.288	18326_s_at	1	2	-1	3	0	-3
ACHI	12852_s_at	16	-6	9	9	8	-10
AC005560.147	12758_at	2	1	1	10	3	3
X98320.2	18312_s_at	1	-2	1	5	-2	0
AC002391.150	17843_s_at	416	-53	487	239	184	63
AC005967.50	17864_at	8	8	5	10	5	0
AC007060.34	19840_s_at	-80	169	106	105	-2	50
BCHI	13211_s_at	44	-94	-1	-13	37	-54
AC001645.19	15965_at	-24	-3	-22	-4	25	-27
AB023448.2	12332_s_at	127	-172	9	-10	9	-133
AC001645.47	15996_at	5	-10	6	-6	29	-20

Accession	Affy id	Cold Leaf3	Cold Leaf 27	Man Leaf 3	Man Leaf 27	Salt Leaf 3	Salt Leaf 27
AL049500.57	16914_s_at	265	-341	19	-7	78	-354
AC007584.48	20194_at	27	182	78	62	30	32

Table 10A-D summarize the root genes up- or down-regulated in response to cold, mannitol or salt stress.

Table 10A:

Accession #	Affy #	Description
<b>Acute (3 hr) manitol stress response downregulated root genes</b>		
AC006577.16	12778_r_at	" gblAAD25772.1 AC006577_8 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gblT44453, gblT04815, gblT45993, gblR30138, gblAI099570 and gblT22281 come from this gene. [Arabidopsis thaliana]"
X98808.1	15985_at	emblCAA67340.1  (X98808) peroxidase ATP3a [Arabidopsis thaliana]
ATU57320	15137_s_at	gblAAB47973.1  (U57320) blue copper-binding protein II [Arabidopsis thaliana]
U81294.2	20421_at	emblCAB10242.1  (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
Z97338.321	16045_s_at	emblCAB10318.1  (Z97338) HSR201 like protein [Arabidopsis thaliana]
ATU62330	15623_f_at	dbj BAA21503.1  (D86591) inorganic phosphate transporter [Arabidopsis thaliana]
AC006577.16	12779_f_at	" gblAAD25772.1 AC006577_8 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gblT44453, gblT04815, gblT45993, gblR30138, gblAI099570 and gblT22281 come from this gene. [Arabidopsis thaliana]"
X98855.2	16028_at	emblCAA67361.1  (X98855) peroxidase ATP8a [Arabidopsis thaliana]
AF128395.12	20395_at	" gblAAD17355.1  (AF128395) contains similarity to pathogenesis-related protein 1 precursors and SCP-like extracellular proteins (Pfam: PF00188, Score=79.8, E=4.1e-21, N=1) [Arabidopsis thaliana]"
Z97340.345	17485_s_at	" emblCAB10405.1  (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]"
ATU10034	15120_s_at	gblAAA93132.1  (U10034) glutamate decarboxylase [Arabidopsis thaliana]



Accession #	Affy #	Description
AC004521.114	19195_at	gblAAC16105.1l (AC004521) unknown protein [Arabidopsis thaliana]
X98319.2	16971_s_at	emblCAA66963.1l (X98319) peroxidase [Arabidopsis thaliana]
X98322.2	17942_s_at	emblCAA66966.1l (X98322) peroxidase [Arabidopsis thaliana]
U81294.2	20422_g_at	emblCAB10242.1l (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
AL049730.104	18983_s_at	emblCAB41721.1l (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
ATPIN2	12932_s_at	gblAAC84042.1l (AF087459) polar-auxin-transport efflux component AGRVITROPIC 1 [Arabidopsis thaliana]
X67421.3	16489_at	emblCAA47807.1l (X67421) extA [Arabidopsis thaliana]
AC004683.79	16461_i_at	gblAAC28766.1l (AC004683) peroxidase [Arabidopsis thaliana]
AC004005.104	19390_at	gblAAC23409.1l (AC004005) unknown protein [Arabidopsis thaliana]
AC004521.119	20608_s_at	gblAAC16106.1l (AC004521) hypothetical protein [Arabidopsis thaliana]
<b>Manitol stress response upregulated in root genes only (acute response)</b>		
AL080253.32	19415_at	emblCAB45805.1l (AL080253) putative protein [Arabidopsis thaliana]
A71596.1	14016_s_at	emblCAB42592.1l (A71596) unnamed protein product [Arabidopsis thaliana]
AC001645.19	15965_at	gblAAB63631.1l (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
A71588.1	14015_s_at	emblCAB42586.1l (A71588) unnamed protein product [Arabidopsis thaliana]

Accession #	Affy #	Description
AC002333.199	13552_at	gblAAB64045.1  (AC002333) endochitinase isolog [Arabidopsis thaliana]
X74514.2	20238_at	emblCAA52620.1  (X74515) beta-fructofuranosidase [Arabidopsis thaliana]
AC001645.47	15996_at	gblAAB63634.1  (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
ATAJ2596	16085_s_at	emblCAB16787.1  (Z99707) patatin-like protein [Arabidopsis thaliana]
AC007135.23	20176_at	gblAAD26967.1 AC007135_3 (AC007135) unknown protein [Arabidopsis thaliana]
X98320.2	18312_s_at	emblCAA67310.1  (X98774) peroxidase ATP6a [Arabidopsis thaliana]
Z99707.288	18326_s_at	emblCAB16788.1  (Z99707) patatin-like protein [Arabidopsis thaliana]
BCHI	13211_s_at	dbj BAA82825.1  (AB023463) basic endochitinase [Arabidopsis thaliana]
AC005560.147	12758_at	gblAAC67329.1  (AC005560) putative major latex protein [Arabidopsis thaliana]
AL049500.57	16914_s_at	emblCAB39936.1  (AL049500) osmotin precursor [Arabidopsis thaliana]
AB023448.2	12332_s_at	dbj BAA82810.1  (AB023448) basic endochitinase [Arabidopsis thaliana]
AL035538.245	16514_at	emblCAB37548.1  (AL035538) putative protein [Arabidopsis thaliana]
AC007584.48	20194_at	gblAAD32907.1 AC007584_5 (AC007584) unknown protein [Arabidopsis thaliana]

Table 10B:

Accession #	Affy #	Description
<b>Salt stress acute response down regulated root only</b>		
AC006577.16	12778_r_at	" gblAAD25772.1 AC006577_8 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSE-motif family. ESTs gblT44453, gblT04815, gblT45993, gblR30138, gblAI099570 and gblT22281 come from this gene. [Arabidopsis thaliana]"
ATU57320	15137_s_at	gblAAB47973.1  (U57320) blue copper-binding protein II [Arabidopsis thaliana]
X98808.1	15985_at	embCAA67340.1  (X98808) peroxidase ATP3a [Arabidopsis thaliana]
U81294.2	20421_at	embCAB10242.1  (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
Z97338.321	16045_s_at	embCAB10318.1  (Z97338) HSR201 like protein [Arabidopsis thaliana]
X98855.2	16028_at	embCAA67361.1  (X98855) peroxidase ATP8a [Arabidopsis thaliana]
AC006577.16	12779_f_at	" gblAAD25772.1 AC006577_8 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSE-motif family. ESTs gblT44453, gblT04815, gblT45993, gblR30138, gblAI099570 and gblT22281 come from this gene. [Arabidopsis thaliana]"
X78586.2	16048_at	embCAA55323.1  (X78586) Dr4 [Arabidopsis thaliana]
ATU62330	15623_f_at	dbj BAA21503.1  (D86591) inorganic phosphate transporter [Arabidopsis thaliana]
AC005560.136	16016_at	gblAAC67328.1  (AC005560) putative major latex protein [Arabidopsis thaliana]
AF098630.3	19118_s_at	embCAB41725.1  (AL049730) putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A) [Arabidopsis thaliana]
AF128395.12	20395_at	" gblAAD17355.1  (AF128395) contains similarity to pathogenesis-related protein 1 precursors and SCP-like extracellular proteins (Pfam: PF00188, Score=79.8, E=4.1e-21, N=1) [Arabidopsis thaliana]"
Z97340.345	17485_s_at	" embCAB10405.1  (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]"

Accession #	Affy #	Description
AL035538.245	16514_at	emblCAB37548.1l (AL035538) putative protein [Arabidopsis thaliana]
X98322.2	17942_s_at	emblCAA66966.1l (X98322) peroxidase [Arabidopsis thaliana]
ATU10034	15120_s_at	gblAAA93132.1l (U10034) glutamate decarboxylase [Arabidopsis thaliana]
AL049730.104	18983_s_at	emblCAB41721.1l (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
AJ133036.5	15969_s_at	emblCAA67313.1l (X98777) peroxidase ATP16a [Arabidopsis thaliana]
U72155.2	15954_at	gblAAB64244.1l (U72155) beta-glucosidase [Arabidopsis thaliana]
X98319.2	16971_s_at	emblCAA66963.1l (X98319) peroxidase [Arabidopsis thaliana]
U81294.2	20422_g_at	emblCAB10242.1l (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
X67421.3	16489_at	emblCAA47807.1l (X67421) extA [Arabidopsis thaliana]
ATPIN2	12932_s_at	gblAAC84042.1l (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana]
AC005310.6	17697_at	gblAAC33493.1l (AC005310) unknown protein [Arabidopsis thaliana]
AC007135.23	20176_at	gblAAD26967.1lAC007135_3 (AC007135) unknown protein [Arabidopsis thaliana]
<b>Salt stress acute response up regulated root only</b>		
AC005967.50	17864_at	gblAAD03387.1l (AC005967) unknown protein [Arabidopsis thaliana]
AC007060.34	19840_s_at	gblAAD25759.1lAC007060_17 (AC007060) Strong similarity to F19I3.2 gil3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gblAC004238. EST gblR90518 comes from this gene.
BCHI	13211_s_at	dbjlBAA82825.1l (AB023463) basic endochitinase [Arabidopsis thaliana]

Accession #	Affy #	Description
AC001645.19	15965_at	gblAAB63631.1  (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
AB023448.2	12332_s_at	dbj BAA82810.1  (AB023448) basic endochitinase [Arabidopsis thaliana]
AC001645.47	15996_at	gblAAB63634.1  (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
AL049500.57	16914_s_at	emblCAB39936.1  (AL049500) osmotin precursor [Arabidopsis thaliana]
AC007584.48	20194_at	gblAAD32907.1 AC007584_5 (AC007584) unknown protein [Arabidopsis thaliana]

Table 10C:

Accession #	Affy #	Description
<b>Genes expressed in root that have no acute response to stress</b>		
X98321.2	19595_s_at	emblCAA66965.1  (X98321) peroxidase [Arabidopsis thaliana]
AC006216.26	18571_at	gblAAD12681.1  (AC006216) Similar to gil3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gblAC004747. ESTs gbl65870 and gblT20812 come from this gene.
AC006216.22	14050_at	" gblAAD12679.1  (AC006216) Similar to gil3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gblAC004747. ESTs gblT44298, gblT42447, gblR64761 and gblI100206 come from this gene."
AL080253.32	19415_at	emblCAB45805.1  (AL080253) putative protein [Arabidopsis thaliana]
X74514.2	20239_g_at	emblCAA52620.1  (X74515) beta-fructofuranosidase [Arabidopsis thaliana]
AC002333.210	13153_r_at	gblAAB64320.1  (AC002335) endochitinase isolog [Arabidopsis thaliana]
CAFFEROYLCO AMETHYLTRAN S	13215_s_at	gblAAA62426.1  (L40031) S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
ATHORF	16649_s_at	gblAAA62426.1  (L40031) S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
AC003673.201	16481_s_at	gblAAC09031.1  (AC003673) peroxidase ATP22a [Arabidopsis thaliana]
AL049638.193	20029_at	emblCAB40949.1  (AL049638) putative DNA-binding protein [Arabidopsis thaliana]

Figure 10D:

Accession #	Affy #	Description
<b>Down regulated with cold stress in root (acute response 3 hrs)</b>		
X98808.1	15985_at	emblCAA67340.1  (X98808) peroxidase ATP3a [Arabidopsis thaliana]
AC006577.16	12778_r_at	" gblAAD25772.1 AC006577_8 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSDL-motif family. ESTs gblT44453, gblT04815, gblT45993, gblR30138, gblAI099570 and gblT22281 come from this gene. [Arabidopsis thaliana]"
ATU62330	15623_f_at	dbj BAA21503.1  (D86591) inorganic phosphate transporter [Arabidopsis thaliana]
Z97338.321	16045_s_at	emblCAB10318.1  (Z97338) HSR201 like protein [Arabidopsis thaliana]
AC006577.16	12779_f_at	" gblAAD25772.1 AC006577_8 (AC006577) Belongs to the PF00657 Lipase/Acylhydrolase with GDSDL-motif family. ESTs gblT44453, gblT04815, gblT45993, gblR30138, gblAI099570 and gblT22281 come from this gene. [Arabidopsis thaliana]"
X98855.2	16028_at	emblCAA67361.1  (X98855) peroxidase ATP8a [Arabidopsis thaliana]
AC004521.114	19195_at	gblAAC16105.1  (AC004521) unknown protein [Arabidopsis thaliana]
X98319.2	16971_s_at	emblCAA66963.1  (X98319) peroxidase [Arabidopsis thaliana]
X98322.2	17942_s_at	emblCAA66966.1  (X98322) peroxidase [Arabidopsis thaliana]
AC001645.19	15965_at	gblAAB63631.1  (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
AJ133036.5	15969_s_at	emblCAA67313.1  (X98777) peroxidase ATP16a [Arabidopsis thaliana]
AF128395.12	20395_at	" gblAAD17355.1  (AF128395) contains similarity to pathogenesis-related protein 1 precursors and SCP-like extracellular proteins (Pfam: PF00188, Score=79.8, E=4.1e-21, N=1) [Arabidopsis thaliana]"
AL080282.74	18597_at	emblCAB45881.1  (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]

Accession #	Affy #	Description
AC002333.199	13552_at	gblAAB64045.1l (AC002333) endochitinase isolog [Arabidopsis thaliana]
AC004521.119	20608_s_at	gblAAC16106.1l (AC004521) hypothetical protein [Arabidopsis thaliana]
A71597.1	12079_s_at	emblCAB42613.1l (A71641) unnamed protein product [Arabidopsis thaliana]
ATPIN2	12932_s_at	gblAAC84042.1l (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana]
AL024486.185	16299_at	emblCAA19705.1l (AL024486) putative protein [Arabidopsis thaliana]
AC001645.47	15996_at	gblAAB63634.1l (AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
AC004684.165	17907_s_at	gblAAC23645.1l (AC004684) unknown protein [Arabidopsis thaliana]
AC004683.79	16461_i_at	gblAAC28766.1l (AC004683) peroxidase [Arabidopsis thaliana]
A71588.1	14015_s_at	emblCAB42586.1l (A71588) unnamed protein product [Arabidopsis thaliana]
<b>Upregulated in root with cold stress</b>		
AL035538.245	16514_at	emblCAB37548.1l (AL035538) putative protein [Arabidopsis thaliana]
AF098630.3	19118_s_at	emblCAB41725.1l (AL049730) putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A) [Arabidopsis thaliana]
AC007584.48	20194_at	gblAAD32907.1lAC007584_5 (AC007584) unknown protein [Arabidopsis thaliana]
X74514.2	20238_at	emblCAA52620.1l (X74515) beta-fructofuranosidase [Arabidopsis thaliana]
AL049730.104	18983_s_at	emblCAB41721.1l (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
X67421.3	16489_at	emblCAA47807.1l (X67421) extA [Arabidopsis thaliana]



Accession #	Affy #	Description
AC007060.34	19840_s_at	gblAAD25759.1 AC007060_17 (AC007060) Strong similarity to F19I3.2 gil3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gblAC004238. EST gblR90518 comes from this gene.

Table 11 provides a description of the corresponding genes for *Arabidopsis* promoters which were constitutively expressed.

Table 11:

Gene ID	Accession # on chip	Affy #	Description
A45785.1_S_AT	A45785.1	19852_s_at	emb CAA02840.1  (A45785) unnamed protein product [Arabidopsis thaliana]
AB003522.2_AT	AB003522.2	12381_at	dbj BAA84392.1  (AP000423) ATPase beta subunit [Arabidopsis thaliana]
AB004872.6_S_AT	AB004872.6	15997_s_at	dbj BAA23547.1  (AB004872) COR47 [Arabidopsis thaliana]
AB005560_S_AT	AB004872.6	15630_s_at	dbj BAA22504.1  (AB005560) AtGDI2 [Arabidopsis thaliana]
AB006693.1_AT	AB006693.1	17438_at	dbj BAA24536.1  (AB006693) spermidine synthase [Arabidopsis thaliana]
AB008105_S_AT	AB008105	17044_s_at	dbj BAA32420.1  (AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]
AB008487_S_AT	AB008487	15127_s_at	dbj BAA31143.1  (AB010915) response regulator1 [Arabidopsis thaliana]
AB008854_S_AT	AB008854	14719_s_at	dbj BAA25248.1  (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
AB010946_S_AT	AB010946	15200_s_at	dbj BAA24804.1  (AB010946) AtRer1B [Arabidopsis thaliana]
AB011545_S_AT	AB011545	15163_s_at	dbj BAA32735.1  (AB011545) GF14 mu [Arabidopsis thaliana]
AB017643_S_AT	AB017643	15164_s_at	gb AAC14411.1  (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AB021858_S_AT	AB021858	16540_s_at	dbj BAA77759.1  (AB021858) plastid heme oxygenase [Arabidopsis thaliana]
AB024282_S_AT	AB024282	15128_s_at	emblCAB71074.1  (AL132962) cysteine synthase AtcysC1 [Arabidopsis thaliana]
AB027151.2_S_AT	AB027151.2	19179_s_at	emblCAB43659.1  (AL050352) threonine synthase [Arabidopsis thaliana]
AC000103.25_S_AT	AC000103.25	20709_s_at	gblAAB61517.1  (AC000103) F21J9.25 [Arabidopsis thaliana]
AC000104.10_R_AT	AC000104.10	13076_r_at	gblAAB70426.1  (AC000104) Strong similarity to 60S ribosomal protein L17 (gblX01694). EST gblAA042332 comes from this gene. [Arabidopsis thaliana]
AC000104.26_AT	AC000104.26	12771_at	gblAAB70434.1  (AC000104) F19P19.13 [Arabidopsis thaliana]
AC000106.13_S_AT	AC000106.13	17900_s_at	gblAAB70401.1  (AC000106) Similar to Glycine SRC2 (gblAB000130). ESTs gblH76869,gblT21700,gblATTS50 89 come from this gene. [Arabidopsis thaliana]
AC000132.16_S_AT	AC000132.16	16531_s_at	gblAAC33220.1  (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana] gblAA395597,gblATTS5197 come from this gene. [Arabidopsis thaliana]
AC000132.6_AT	AC000132.6	16420_at	gblAAB60721.1  (AC000132) Similar to elongation factor 1- gamma (gblEF1G_XENLA). ESTs gblT20564,gblT45940,gblT04527 come from this gene. [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AC002131.48_S_AT	AC002131.48	12750_s_at	gblAAC17620.1l (AC002131) Identical to aspartic proteinase cDNA gblU51036 from A. thaliana. ESTs gblN96313, gblT21893, gblR30158, gblT21482, gblT43650, gblR64749, gblR65157, gblT88269, gblT44552, gblT22542, gblT76533, gblT44350, gblZ34591, gblAA728734, g
AC002329.46_AT	AC002329.46	13074_at	emblCAA54095.1l (X76651) ribosomal protein S4 [Solanum tuberosum]
AC002330.39_AT	AC002330.39	13574_at	gblAAC78269.1lAAC78269 (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
AC002332.100_AT	AC002332.100	13105_at	gblAAB80655.1l (AC002332) 60S ribosomal protein L23 [Arabidopsis thaliana]
AC002332.71_AT	AC002332.71	17435_at	gblAAB80652.1l (AC002332) putative PRP19-like spliceosomal protein [Arabidopsis thaliana]
AC002334.110_G_AT	AC002334.110	16940_g_at	gblAAC04922.1l (AC002334) putative synaptobrevin [Arabidopsis thaliana]
AC002336.101_G_AT	AC002336.101	12809_g_at	gblAAB87594.1l (AC002336) 40S ribosomal protein S26 [Arabidopsis thaliana]
AC002339.51_AT	AC002339.51	16507_at	gblAAC02764.1l (AC002339) 40S ribosomal protein S2 [Arabidopsis thaliana]
AC002343.3_AT	AC002343.3	16447_at	gblAAB63606.1l (AC002343) HSP90 isolog [Arabidopsis thaliana]
AC002521.146_AT	AC002521.146	16917_at	gblAAC05346.1l (AC002521) putative ubiquitin-conjugating enzyme E2 [Arabidopsis

Gene ID	Accession # on chip	Affy #	Description
AC002561.51_AT	AC002561.51	18655_at	gblAAB88646.1l (AC002561) unknown protein [Arabidopsis thaliana]
AC003672.64_S_AT	AC003672.64	20425_s_at	gblAAC27463.1l (AC003672) putative small GTP-binding protein [Arabidopsis thaliana]
AC003981.34_S_AT	AC003981.34	16523_s_at	gblAAC14060.1l (AC003981) F22O13.34 [Arabidopsis thaliana]
AC004077.166_S_AT	AC004077.166	17004_s_at	gblAAC26708.1l (AC004077) 60S ribosomal protein L18A [Arabidopsis thaliana]
AC004165.105_AT	AC004165.105	13125_at	gblAAC16961.1l (AC004165) putative ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]
AC004218.83_S_AT	AC004218.83	13616_s_at	gblAAC27837.1l (AC004218) 60S ribosomal protein L23A [Arabidopsis thaliana]
AC004393.22_AT	AC004393.22	16953_at	gblAAC18792.1l (AC004393) Similar to ribosomal protein L17 gblX62724 from Hordeum vulgare. ESTs gblZ34728, gblF19974, gblT75677 and gblZ33937 come from this gene. [Arabidopsis thaliana]
AC004401.119_AT	AC004401.119	13594_at	gblAAC17825.1l (AC004401) unknown protein [Arabidopsis thaliana]
AC004401.140_AT	AC004401.140	12767_at	gblAAB87096.2l (AC002391) unknown protein [Arabidopsis thaliana]
AC004450.11_AT	AC004450.11	18882_at	gblAAC64298.1l (AC004450) 3-isopropylmalate dehydratase, small subunit [Arabidopsis thaliana]
AC004450.83_AT	AC004450.83	18262_at	gblAAC64306.1l (AC004450) unknown protein [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AC004481.84_AT	AC004481.84	13102_at	gblAAC27401.1  (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]
AC004557.10_AT	AC004557.10	17436_at	gblAAC80610.1  (AC004557) F17L21.10 [Arabidopsis thaliana]
AC004557.20_AT	AC004557.20	17374_at	gblAAC80620.1  (AC004557) F17L21.20 [Arabidopsis thaliana]
AC004557.8_AT	AC004557.8	18874_at	gblAAC80608.1  (AC004557) F17L21.8 [Arabidopsis thaliana]
AC004665.121_S_AT	AC004665.121	18629_s_at	gblAAC28542.1  (AC004665) remorin [Arabidopsis thaliana]
AC004665.31_S_AT	AC004665.31	15977_s_at	gblAAC28529.1  (AC004665) aquaporin (plasma membrane intrinsic protein 1B) [Arabidopsis thaliana]
AC004669.34_AT	AC004669.34	16430_at	gblAAC20720.1  (AC004669) glutathione S-transferase [Arabidopsis thaliana]
AC004747.160_S_AT	AC004747.160	15506_s_at	gblAAC31239.1  (AC004747) unknown protein [Arabidopsis thaliana]
AC005169.214_AT	AC005169.214	18221_at	gblAAC62141.1  (AC005169) 40S ribosomal protein S30 [Arabidopsis thaliana]
AC005169.221_AT	AC005169.221	18283_at	gblAAC62149.1  (AC005169) putative ribosomal protein L28 [Arabidopsis thaliana]
AC005287.20_S_AT	AC005287.20	16027_s_at	gblAAD25605.1 AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]
AC005287.52_AT	AC005287.52	14073_at	No hits found less than or equal to 1e-15.
AC005309.201_I_AT	AC005309.201	15570_i_at	gblAAC63650.1  (AC005309) unknown protein [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AC005309.64_S_AT	AC005309.64	16009_s_at	gblAAC63629.11 (AC005309) glutathione S-transferase (GST6) [Arabidopsis thaliana]
AC005388.6_S_AT	AC005388.6	12783_s_at	gblAAC64875.11 (AC005388) Identical to gblL14814 DNA for tissue-specific acyl carrier protein isoform 2 from A. thaliana. ESTs gblAA597351, gblT41805, gblH36871, gblR30210, gblAA042549, gblZ47650, gblH76304 and gblAA597348 come from this gene. [Arabidops
AC005397.40_S_AT	AC005397.40	16471_s_at	gblAAC62877.11 (AC005397) eukaryotic translation initiation factor 3 delta subunit [Arabidopsis thaliana]
AC005662.30_S_AT	AC005662.30	16952_s_at	gblAAC78532.11 (AC005662) calmodulin-like protein [Arabidopsis thaliana]
AC005679.10_S_AT	AC005679.10	12775_s_at	gblAAC83021.11 (AC005679) Identical to gblU65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gblN96435, gblN96106, gblN96189, gblN96091, gblAA042286, gblF14324, gblW43643, gblN96027, gblN96299, gblR29943, gblT43460, gblT43544, gblT2247
AC005727.191_AT	AC005727.191	16901_at	gblAAC79595.11 (AC005727) unknown protein [Arabidopsis thaliana]
AC005824.107_AT	AC005824.107	16527_at	gblAAC73028.11 (AC005824) 60S acidic ribosomal protein P2 [Arabidopsis thaliana]
AC005824.114_AT	AC005824.114	17910_at	gblAAC73029.11 (AC005824) 60S acidic ribosomal protein P2 [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AC005824.21_AT	AC005824.21	13089_at	gblAAC73015.1l (AC005824) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
AC005896.150_S_AT	AC005896.150	18603_s_at	gblAAC98060.1l (AC005896) putative protein translocase [Arabidopsis thaliana]
AC005897.156_S_AT	AC005897.156	13572_s_at	gblAAC97246.1l (AC005897) 10-formyltetrahydrofolate synthetase [Arabidopsis thaliana]
AC005936.95_AT	AC005936.95	16416_at	gblAAC97221.1l (AC005936) protease inhibitor II [Arabidopsis thaliana]
AC005990.10_AT	AC005990.10	13069_at	gblAAC98042.1l (AC005990) Strong similarity to gblM95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gblZ25826, gblR90191, gblN65697, gblAA713150, gblT46332, gblAA040967, gblAA712956, gblT46403, gblT46050, gblAI100391 and gblZ25043 come from
AC006068.93_AT	AC006068.93	18645_at	gblAAD15447.1l (AC006068) unknown protein [Arabidopsis thaliana]
AC006085.15_AT	AC006085.15	20562_at	gblAAD30634.1lAC006085_7 (AC006085) Unknown protein [Arabidopsis thaliana]
AC006200.119_AT	AC006200.119	13132_at	gblAAD14525.1l (AC006200) 60S ribosomal protein L7 [Arabidopsis thaliana]
AC006201.107_S_AT	AC006201.107	16924_s_at	gblAAD20124.1l (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
AC006223.65_AT	AC006223.65	14089_at	gblAAD15390.1l (AC006223) putative hydrolase [Arabidopsis thaliana]



Gene ID	Accession # on chip	Affy #	Description
AC006234.156_AT	AC006234.156	14099_at	gblAAD20913.1l (AC006234) unknown protein [Arabidopsis thaliana]
AC006260.52_AT	AC006260.52	12769_at	gblAAD18142.1l (AC006260) aquaporin (plasma membrane intrinsic protein 2B) [Arabidopsis thaliana]
AC006264.30_AT	AC006264.30	13095_at	gblAAD29800.1lAC006264_8 (AC006264) putative signal sequence receptor, alpha subunit
AC006300.112_AT	AC006300.112	16948_at	gblAAD20708.1l (AC006300) putative glucose regulated repressor protein [Arabidopsis thaliana]
AC006300.70_AT	AC006300.70	16487_at	gblAAD20704.1l (AC006300) putative dioxygenase [Arabidopsis thaliana]
AC006403.110_AT	AC006403.110	18223_at	gblAAD18124.1l (AC006403) unknown protein [Arabidopsis thaliana]
AC006438.21_AT	AC006438.21	12749_at	gblAAD41971.1lAC006438_3 (AC006438) similar to cold acclimation protein WCOR413 [Triticum aestivum] [Arabidopsis thaliana]
AC006526.57_AT	AC006526.57	14103_at	No hits found less than or equal to 1e-15.
AC006532.47_AT	AC006532.47	19940_at	gblAAD20090.1l (AC006532) putative endosomal protein [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AC006577.32_AT	AC006577.32	16941_at	gblAAD25780.1 AC006577_16 (AC006577) Similar to gblU55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PFI00076 RNA recognition motif domains. ESTs gblT21032 and gblT44127 come from this gene. [Arabidopsis thaliana]
AC006585.146_AT	AC006585.146	14565_at	gblAAD23019.1 AC006585_14 (AC006585) putative steroid binding protein [Arabidopsis thaliana]
AC006586.141_AT	AC006586.141	17390_at	gblAAD22696.1 AC006586_5 (AC006586) 40S ribosomal protein S16 [Arabidopsis thaliana]
AC006592.150_S_AT	AC006592.150	15980_s_at	emb CAA47427.1  (X67034) Athb-6 [Arabidopsis thaliana]
AC006841.122_AT	AC006841.122	19650_at	gblAAD23699.1 AC006841_15 (AC006841) coatomer alpha subunit [Arabidopsis thaliana]
AC006919.140_AT	AC006919.140	12742_at	gblAAD24635.1 AC006919_15 (AC006919) enolase (2-phospho-D-glycerate hydrolyase) [Arabidopsis
AC006919.171_AT	AC006919.171	13070_at	gblAAD24640.1 AC006919_20 (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
AC006921.52_AT	AC006921.52	16511_at	gblAAD21434.1  (AC006921) unknown protein [Arabidopsis thaliana]
AC006922.106_AT	AC006922.106	12412_at	gblAAD31573.1 AC006922_5 (AC006922) putative s-adenosylmethionine synthetase [Arabidopsis thaliana]
AC006922.28_S_AT	AC006922.28	15962_s_at	gblAAD31569.1 AC006922_1 (AC006922) putative aquaporin (tonoplast intrinsic protein gamma)

Gene ID	Accession # on chip	Affy #	Description
AC006929.77_AT	AC006929.77	13150_at	gblAAD21502.1l (AC006929) putative rubisco subunit binding-protein alpha subunit [Arabidopsis thaliana]
AC006951.208_S_AT	AC006951.208	13107_s_at	gblAAD25839.1lAC006951_18 (AC006951) 40S ribosomal protein S17 [Arabidopsis thaliana]
AC007017.278_S_AT	AC007017.278	20024_s_at	gblAAD21476.1l (AC007017) unknown protein [Arabidopsis thaliana]
AC007019.105_AT	AC007019.105	16022_at	gblAAD20405.1l (AC007019) putative ATP synthase [Arabidopsis thaliana]
AC007070.167_AT	AC007070.167	13166_at	emblCAA64728.1l (X95458) ribosomal protein L39 [Zea mays]
AC007071.72_AT	AC007071.72	16933_at	gblAAD24852.1lAC007071_24 (AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
AC007119.88_AT	AC007119.88	13080_at	gblAAD23647.1lAC007119_13 (AC007119) 40S ribosomal protein S25 [Arabidopsis thaliana]
AC007135.50_AT	AC007135.50	16919_at	gblAAD26971.1lAC007135_8 (AC007135) 40S ribosomal protein S14 [Arabidopsis thaliana]
AC007138.25_S_AT	AC007138.25	12797_s_at	gblAAD22647.1lAC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]
AC007170.48_AT	AC007170.48	17857_at	gblAAD25640.1lAC007170_2 (AC007170) cytoplasmic aconitate hydratase [Arabidopsis thaliana]
AC007195.93_I_AT	AC007195.93	16969_i_at	gblAAA99933.1l (L44581) vacuolar H <sup>+</sup> -pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AC007357.17_S_AT	AC007357.17	13104_s_at	emblCAA74029.1  (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana]
AC007576.5_AT	AC007576.5	12781_at	gblAAD39279.1 AC007576_2 (AC007576) Unknown protein [Arabidopsis thaliana]
AC007659.93_R_AT	AC007659.93	13169_r_at	gblAAD32831.1 AC007659_13 (AC007659) putative GATA-type zinc finger transcription factor [Arabidopsis thaliana]
AF000657.40_AT	AF000657.40	19623_at	gblAAB72175.1  (AF000657) cytochrome C [Arabidopsis thaliana]
AF001394_S_AT	AF001394	15600_s_at	gblAAD00895.1  (AF001394) fatty acid desaturase/cytochrome b5 fusion protein [Arabidopsis thaliana]
AF003096_F_AT	AF003096	14723_f_at	gblAAC49769.1  (AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]
AF003105.1_AT	AF003105.1	17858_at	gblAAC49778.1  (AF003105) AP2 domain containing protein RAP2.12 [Arabidopsis thaliana]
AF004216_S_AT	AF004216	15205_s_at	gblAAC49749.1  (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
AF004393_S_AT	AF004393	14714_s_at	gblAAB62692.1  (AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]
AF013294.25_S_AT	AF013294.25	18650_s_at	gblAAB62867.1  (AF013294) AT0ZI1 gene product [Arabidopsis thaliana]
AF013294.35_AT	AF013294.35	18573_at	gblAAB62855.1  (AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AF013959.4_AT	AF013959.4	16436_at	gblAAB67234.1l (AF013959) metallothionein-like protein [Arabidopsis thaliana]
AF017641_S_AT	AF017641	15165_s_at	gblAAC17844.1l (AF017641) nucleoside diphosphate kinase type 1 [Arabidopsis
AF017991_S_AT	AF017991	15150_s_at	gblAAB97312.1l (AF017991) salt stress inducible small GTP binding protein Ran1
AF027172.3_S_AT	AF027172.3	16906_s_at	gblAAC39334.1l (AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana]
AF027174_S_AT	AF027174	15603_s_at	gblAAC39336.1l (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]
AF034387_S_AT	AF034387	14727_s_at	gblAAC33264.1l (AF034387) AFT protein [Arabidopsis thaliana]
AF034694_S_AT	AF034694	16544_s_at	gblAAB87692.1l (AF034694) ribosomal protein L23a [Arabidopsis thaliana]
AF043519_S_AT	AF043519	15130_s_at	gblAAC95161.1l (AC005970) 20S proteasome subunit (PAA2) [Arabidopsis thaliana]
AF043528_S_AT	AF043528	16546_s_at	gblAAC32064.1l (AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana]
AF044265_S_AT	AF044265	15668_s_at	gblAAC00512.1l (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana]
AF044313_S_AT	AF044313	14717_s_at	gblAAC05742.1l (AF044313) anion channel protein [Arabidopsis thaliana]
AF059294_S_AT	AF059294	14736_s_at	gblAAF26761.1lAC007396_10 (AC007396) T4O12.15 [Arabidopsis thaliana] protein in budding yeast [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AF061519_S_AT	AF061519	15581_s_at	gblAAD10208.1  (AF061519) copper/zinc superoxide dismutase [Arabidopsis thaliana]
AF062485.1_AT	AF062485.1	17468_at	gblAAC29067.1  (AF062485) cellulose synthase [Arabidopsis thaliana]
AF063901_S_AT	AF063901	14737_s_at	gblAAC26854.1  (AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana]
AF069299.19_AT	AF069299.19	16925_at	gblAAC19305.1  (AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]
AF074375_S_AT	AF074375	15114_s_at	gblAAC83240.1  (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]
AF076484_S_AT	AF076484	16627_s_at	gblAAD04627.1  (AF108660) CYT1 protein [Arabidopsis thaliana]
AF076641.2_AT	AF076641.2	16977_at	gblAAD46064.1 AF076641_1 (AF076641) homeodomain leucine-zipper protein ATHB16 [Arabidopsis thaliana]
AF077528_S_AT	AF077528	15152_s_at	gblAAB72116.1  (U69533) AtKAP alpha [Arabidopsis thaliana]
AF080120.11_S_AT	AF080120.11	16935_s_at	gblAAC35545.1  (AF080120) similar to vacuolar ATPases [Arabidopsis thaliana] thaliana]
AF082565_S_AT	AF082565	15639_s_at	gblAAD29109.1 AF082565_1 (AF082565) ATP dependent copper transporter [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AF083336.2_S_AT	AF083336.2	16932_s_at	gblAAD10030.1l (AF083337) ribosomal protein S27 [Arabidopsis thaliana]
AF083337.3_S_AT	AF083337.3	16931_s_at	gblAAD10030.1l (AF083337) ribosomal protein S27 [Arabidopsis thaliana]
AF118822_F_AT	AF118822	16080_f_at	gblAAD20612.1l (AF118822) senescence-associated protein [Arabidopsis thaliana]
AF123253.3_I_AT	AF123253.3	20459_i_at	emblCAB43915.1l (AL078470) AIM1 protein [Arabidopsis thaliana]
AF136152_S_AT	AF136152	15643_s_at	gblAAD39465.1lAF136152_1 (AF136152) PUR alpha-1 [Arabidopsis thaliana]
AF144387_AT	AF144387	12857_at	gblAAD35005.1lAF144387_1 (AF144387) thioredoxin-like 1 [Arabidopsis thaliana]
AF167983_S_AT	AF167983	15210_s_at	gblAAC26685.1l (AC004077) putative pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]
AF181688_R_AT	AF181688	17994_r_at	gblAAF24609.1lAC010870_2 (AC010870) vacuolar membrane ATPase subunit G (AVMA10) [Arabidopsis thaliana]
AF181966_AT	AF181966	17996_at	gblAAD55787.1lAF181966_1 (AF181966) methylenetetrahydrofolate reductase MTHFR1 [Arabidopsis thaliana]
AF186847_S_AT	AF186847	18000_s_at	gblAAF03749.1lAF186847_1 (AF186847) TIM17 [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AGO1_S_AT	AGO1	12877_s_at	gb AAD49755.1 AC007932_3 (AC007932) Identical to gb U91995 Argonaute protein from Arabidopsis
AJ001342.2_S_AT	AJ001342.2	16923_s_at	embl CAA18846.1  (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]
AJ001397_S_AT	AJ001397	18011_s_at	dbj BAA22504.1  (AB005560) AtGDI2 [Arabidopsis thaliana]
AJ006787.1_AT	AJ006787.1	19224_at	embl CAA07251.1  (AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]
AJ010456.2_AT	AJ010456.2	17470_at	embl CAA09195.1  (AJ010456) RNA helicase [Arabidopsis thaliana]
AJ010505_S_AT	AJ010505	18018_s_at	embl CAB54830.1  (AJ010505) cysteine synthase [Arabidopsis thaliana]
AJ011628_I_AT	AJ011628	18032_i_at	embl CAB56580.1  (AJ011628) squamosa promoter binding protein-like 1 [Arabidopsis thaliana]
AJ012571.2_S_AT	AJ012571.2	16012_s_at	embl CAA10060.1  (AJ012571) glutathione transferase [Arabidopsis thaliana]
AJ131205_AT	AJ131205	18047_at	embl CAA10320.1  (AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]
AL021636.178_AT	AL021636.178	16499_at	embl CAA16587.1  (AL021636) putative protein [Arabidopsis thaliana]
AL021687.199_AT	AL021687.199	19677_at	embl CAA16709.1  (AL021687) putative protein [Arabidopsis thaliana]



Gene ID	Accession # on chip	Affy #	Description
AL021712.156_AT	AL021712.156	20559_at	emblCAA16781.1  (AL021712) putative protein [Arabidopsis thaliana]
AL021811.156_AT	AL021811.156	12776_at	emblCAA16969.1  (AL021811) putative protein [Arabidopsis thaliana]
AL021890.14_AT	AL021890.14	13591_at	emblCAA17148.1  (AL021890) putative protein [Arabidopsis thaliana]
AL021890.209_S_AT	AL021890.209	12752_s_at	emblCAA17163.1  (AL021890) peroxidase prxr1 [Arabidopsis thaliana]
AL022023.145_S_AT	AL022023.145	16905_s_at	emblCAA17773.1  (AL022023) catalase [Arabidopsis thaliana]
AL022141.10_S_AT	AL022141.10	16976_s_at	emblCAA18507.1  (AL022373) ribosomal protein L2 [Arabidopsis thaliana]
AL022224.182_S_AT	AL022224.182	16021_s_at	emblCAA18251.1  (AL022224) endomembrane-associated protein [Arabidopsis thaliana]
AL022224.72_AT	AL022224.72	13122_at	emblCAA18240.1  (AL022224) putative protein [Arabidopsis thaliana]
AL022373.153_AT	AL022373.153	12802_at	emblCAA18498.1  (AL022373) DnaJ-like protein [Arabidopsis thaliana]
AL022580.188_AT	AL022580.188	17878_at	emblCAA18628.1  (AL022580) putative pectinacylesterase protein [Arabidopsis thaliana]
AL023094.216_S_AT	AL023094.216	12234_s_at	emblCAA18841.1  (AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]
AL023094.323_S_AT	AL023094.323	16515_s_at	emblCAA18849.1  (AL023094) putative protein [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AL031326.138_AT	AL031326.138	17931_at	emblCAA20461.1  (AL031326) water channel-like protein [Arabidopsis thaliana]
AL034567.189_AT	AL034567.189	13088_at	emblCAA22574.1  (AL034567) ubiquinol-cytochrome c reductase- like protein [Arabidopsis thaliana]
AL035356.123_AT	AL035356.123	13097_at	emblCAA22994.1  (AL035356) putative protein [Arabidopsis thaliana]
AL035394.117_AT	AL035394.117	17384_at	emblCAA23029.1  (AL035394) putative protein [Arabidopsis thaliana]
AL035440.191_S_AT	AL035440.191	13133_s_at	emblCAB36530.1  (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
AL035440.447_AT	AL035440.447	17011_at	emblCAB36546.1  (AL035440) putative DNA binding protein [Arabidopsis thaliana]
AL035440.66_AT	AL035440.66	18661_at	emblCAB36517.1  (AL035440) putative protein [Arabidopsis thaliana]
AL035526.101_S_AT	AL035526.101	13073_s_at	emblCAB37458.1  (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]
AL035540.348_S_AT	AL035540.348	19961_s_at	gblAAB24074.1  (S47408) glycine- rich protein, atGRP {clone atGRP- 2} [Arabidopsis
AL035540.94_AT	AL035540.94	12804_at	emblCAB37507.1  (AL035540) probable H <sup>+</sup> -transporting ATPase [Arabidopsis thaliana]
AL035656.126_AT	AL035656.126	17459_at	emblCAB38614.1  (AL035656) putative protein [Arabidopsis thaliana]
AL035679.13_S_AT	AL035679.13	16967_s_at	gblAAA99933.1  (L44581) vacuolar H <sup>+</sup> -pumping ATPase 16 kDa proteolipid [Arabidopsis [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AL035679.232_AT	AL035679.232	18905_at	emblCAB38828.1  (AL035679) putative proton pump [Arabidopsis thaliana]
AL035680.110_S_AT	AL035680.110	17429_s_at	emblCAB38843.1  (AL035680) translation initiation factor [Arabidopsis thaliana]
AL035680.53_AT	AL035680.53	13578_at	emblCAB38839.1  (AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]
AL035709.87_AT	AL035709.87	17389_at	emblCAB38931.1  (AL035709) putative protein [Arabidopsis thaliana]
AL049171.158_AT	AL049171.158	20180_at	No hits found less than or equal to 1e-15.
AL049171.25_AT	AL049171.25	17005_at	emblCAB38952.1  (AL049171) putative ribosomal protein [Arabidopsis thaliana]
AL049480.178_AT	AL049480.178	13940_at	emblCAB39610.1  (AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]
AL049608.184_AT	AL049608.184	12813_at	emblCAB40778.1  (AL049608) putative protein [Arabidopsis thaliana]
AL050300.15_F_AT	AL050300.15	13129_f_at	emblCAB43405.1  (AL050300) ubiquitin / ribosomal protein CEP52 [Arabidopsis thaliana]
AL050300.27_AT	AL050300.27	16920_at	emblCAB43407.1  (AL050300) putative ribosomal protein S14 [Arabidopsis thaliana]
AL050398.4_AT	AL050398.4	19133_at	emblCAB43690.1  (AL050398) H <sup>+</sup> -transporting ATPase-like protein [Arabidopsis thaliana]
AL078464.37_AT	AL078464.37	14108_at	emblCAB43836.1  (AL078464) putative protein [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
AL078468.11_AT	AL078468.11	18330_at	emb CAB43885.1  (AL078468) acyl-CoA synthetase-like protein [Arabidopsis thaliana]
AL078637.47_S_AT	AL078637.47	12803_s_at	emb CAB45057.1  (AL078637) putative protein [Arabidopsis thaliana]
AL096856.7_AT	AL096856.7	13093_at	emb CAB51061.1  (AL096856) B12D-like protein [Arabidopsis thaliana]
AL096860.157_AT	AL096860.157	13079_at	emb CAB51209.1  (AL096860) 40S RIBOSOMAL PROTEIN S20 homolog [Arabidopsis thaliana]
AOS_S_AT	AOS	12881_s_at	emb CAA63266.1  (X92510) allene oxide synthase [Arabidopsis thaliana]
AP000423_AT	AP000423	12847_at	dbj BAA84366.1  (AP000423) orf within trnK intron [Arabidopsis thaliana]
APX3_S_AT	APX3	12885_s_at	emb CAA66640.1  (X98003) ascorbate peroxidase [Arabidopsis thaliana]
ATADHIII_AT	ATADHIII	12893_at	emb CAA57973.1  (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]
ATERF3_S_AT	ATERF3	12906_s_at	dbj BAA32420.1  (AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]
ATHADPRFA_S_AT	ATHADPRFA	15677_s_at	gb AAA32729.1  (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
ATHAVAP_S_AT	ATHAVAP	15191_s_at	gb AAA99933.1  (L44581) vacuolar H <sup>+</sup> -pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
ATHAVAPA_S_AT	ATHAVAPA	15584_s_at	gblAAD26493.1 AC007195_7 (AC007195) putative vacuolar proton-ATPase 16 kDa proteolipid [Arabidopsis thaliana]
ATHAVAPC_S_AT	ATHAVAPC	16145_s_at	gblAAD38803.1 AF153677_1 (AF153677) vacuolar H <sup>+</sup> -pumping ATPase 16 kDa subunit c isoform 4 thaliana]
ATHD12AAA_S_AT	ATHD12AAA	15134_s_at	gblAAA32782.1  (L26296) delta-12 desaturase [Arabidopsis thaliana]
ATHDYNAGTP_S_AT	ATHDYNAGTP	15585_s_at	gblAAB63528.1  (L36939) dynamin-like GTP binding protein [Arabidopsis thaliana]
ATHERD13_S_AT	ATHERD13	15193_s_at	gblAAC20721.1  (AC004669) glutathione S-transferase [Arabidopsis thaliana]
ATHERD15_S_AT	ATHERD15	15104_s_at	gblAAC23728.1  (AC004625) dehydration-induced protein (ERD15) [Arabidopsis thaliana]
ATHGFPSIA_S_AT	ATHGFPSIA	14734_s_at	gblAAA32799.1  (L09110) GF14 psi chain [Arabidopsis thaliana]
ATHHMG1_AT	ATHHMG1	12920_at	gblAAA32814.1  (L19261) hydroxymethylglutaryl CoA reductase [Arabidopsis thaliana]
ATHHMGCOAR_S_AT	ATHHMGCOAR	12921_s_at	emblCAA33139.1  (X15032) hydroxy methylglutaryl CoA reductase (AA 1-592)
ATHMERI5B_S_AT	ATHMERI5B	15614_s_at	emblCAB52471.1  (AL109796) xyloglucan endo-1, 4-beta-D-glucanase precursor [Arabidopsis thaliana]
ATHMTMACP_S_AT	ATHMTMACP	16574_s_at	gblAAB96840.1  (L23574) acyl carrier protein precursor [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
ATHPRPHC_S_AT	ATHPRPHC	15119_s_at	gblAAD10854.1l (U60135) serine/threonine protein phosphatase 2A-3 catalytic
ATHRP28A_S_AT	ATHRP28A	16577_s_at	gblAAA32862.1l (L09755) ribosomal protein S28 [Arabidopsis thaliana]
ATHRPCA_S_AT	ATHRPCA	15155_s_at	gblAAA66160.1l (M32654) ribosomal protein [Arabidopsis thaliana]
ATHSAR1_S_AT	ATHSAR1	15617_s_at	gblAAA56991.1l (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]
ATORNCARB_S_AT	ATORNCARB	15213_s_at	emb/CAA04115.1l (AJ000476) Ornithine carbamoyltransferase [Arabidopsis thaliana]
ATTHIRED2_S_AT	ATTHIRED2	13184_s_at	gblAAC49351.1l (U35640) thioredoxin h [Arabidopsis thaliana]
ATTHIRED3_AT	ATTHIRED3	13185_at	emb/CAA84612.1l (Z35475) thioredoxin [Arabidopsis thaliana]
ATU01955_S_AT	ATU01955	15135_s_at	gblAAF27153.1l/AC016529_16 (AC016529) putative 40S ribosomal protein SA (laminin receptor-like
ATU09137_S_AT	ATU09137	15156_s_at	gblAAA52225.1l (U09137) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]
ATU15108_S_AT	ATU15108	17078_s_at	gblAAA50250.1l (U15108) metallothionein-like protein [Arabidopsis thaliana]
ATU15130_S_AT	ATU15130	15157_s_at	No hits found.
ATU18410_S_AT	ATU18410	16156_s_at	gblAAD15575.1l (AC006340) auxin-regulated protein (IAA8) [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
ATU18675_S_AT	ATU18675	15620_s_at	gblAAD47191.1 AF106084_1 (AF106084) 4-coumarate:CoA ligase 1 [Arabidopsis thaliana]
ATU20347_S_AT	ATU20347	15649_s_at	gblAAA91976.1  (U20347) mRNA corresponding to this gene accumulates in response to
ATU21214_S_AT	ATU21214	15590_s_at	gblAAA86507.1  (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
ATU21557_S_AT	ATU21557	16098_s_at	gblAAC49255.1  (U21557) phosphoprotein phosphatase 2A, regulatory subunit A [Arabidopsis thaliana]
ATU22340_S_AT	ATU22340	15136_s_at	gblAAB49030.1  (U22340) DnaJ homolog [Arabidopsis thaliana]
ATU36765_S_AT	ATU36765	15177_s_at	gblAAC49079.1  (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana]
ATU37235_S_AT	ATU37235	15195_s_at	emblCAB58515.1  (A74281) unnamed protein product [Arabidopsis thaliana]
ATU37281_F_AT	ATU37281	16158_f_at	gblAAB52506.1  (U27811) actin7 [Arabidopsis thaliana]
ATU37587_S_AT	ATU37587	13205_s_at	gblAAC49120.1  (U37587) cell division cycle protein [Arabidopsis thaliana]
ATU39485_S_AT	ATU39485	15122_s_at	gblAAC49281.1  (U39485) delta tonoplast integral protein [Arabidopsis thaliana]
ATU43325_S_AT	ATU43325	15691_s_at	gblAAB39480.1  (U43325) profilin 1 [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
ATU43397_S_AT	ATU43397	15112_s_at	gblAAD09837.1l (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana] and cryptochrome 2 apoprotein (CRY2) (gblU43397). ESTs gblW43661 and gblZ25638 come from this gene. [Arabidopsis thaliana]
ATU46665_S_AT	ATU46665	14730_s_at	gblAAC31617.1l (U49937) glutamate decarboxylase [Arabidopsis thaliana] Arabidopsis thaliana. ESTs gblW43856, gblN37724, gblZ34642 and gblR90491 come from this gene.
ATU49072_S_AT	ATU49072	15215_s_at	gblAAB84353.1l (U49072) IAA16 [Arabidopsis thaliana]
ATU49259_S_AT	ATU49259	15652_s_at	gblAAF26982.1lAC018363_27 (AC018363) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]
ATU52851_S_AT	ATU52851	15197_s_at	gblAAB09723.1l (U52851) arginine decarboxylase [Arabidopsis thaliana]
ATU56929_S_AT	ATU56929	15180_s_at	gblAAB57799.1l (AF001535) AGAA.4 [Arabidopsis thaliana]
ATU63633_S_AT	ATU63633	14721_s_at	gblAAB17665.1l (U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
ATU66343_S_AT	ATU66343	15654_s_at	gblAAC49695.1l (U66343) calreticulin [Arabidopsis thaliana]
ATU68545_S_AT	ATU68545	14722_s_at	gblAAA74737.1l (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana]
ATU75191_S_AT	ATU75191	15216_s_at	gblAAB51576.1l (U75198) germin-like protein [Arabidopsis thaliana]



Gene ID	Accession # on chip	Affy #	Description
ATU77381_S_AT	ATU77381	16106_s_at	gblAAB82647.1l (U77381) WD-40 repeat protein [Arabidopsis thaliana]
ATU78297_F_AT	ATU78297	15100_f_at	gblAAB36949.1l (U78297) plasma membrane intrinsic protein PIP3 [Arabidopsis thaliana]
ATU78870_S_AT	ATU78870	17030_s_at	gblAAB68038.1l (U78866) gene1000 [Arabidopsis thaliana]
ATU79960_S_AT	ATU79960	16056_s_at	gblAAB72112.1l (U79960) vacuolar sorting receptor homolog [Arabidopsis thaliana]
ATU80186_S_AT	ATU80186	15627_s_at	gblAAB86804.1l (U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]
ATU91995_S_AT	ATU91995	16170_s_at	gblAAD49755.1lAC007932_3 (AC007932) Identical to gblU91995 Argonaute protein from Arabidopsis
CATL_S_AT	CATL	13218_s_at	gblAAC17732.1l (AF021937) catalase 3 [Arabidopsis thaliana]
CYSPROL_S_AT	CYSPROL	13230_s_at	emblCAB10398.1l (Z97340) cysteine proteinase like protein [Arabidopsis thaliana]
D01027.1_AT	D01027.1	18940_at	gblAAC24370.1l (U89959) ARA-5 [Arabidopsis thaliana]
D11394.4_S_AT	D11394.4	16011_s_at	emblCAA44630.1l (X62818) Metallothionein-like protein [Arabidopsis thaliana]
D13043.4_AT	D13043.4	15973_at	dbjlbAA02374.1l (D13043) thiol protease [Arabidopsis thaliana]
D83531_S_AT	D83531	15113_s_at	dbjlbAA11944.1l (D83531) GDP dissociation inhibitor [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
D88374_S_AT	D88374	15149_s_at	dbj BAA13599.1  (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis [Arabidopsis thaliana]
GLUTATHIONEPER OXIDASE1_S_AT	GLUTATHIONE PEROXIDASE1	13259_s_at	gb AAD24836.1 AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]
GST1_RC_S_AT	GST1	13263_s_at	emb CAA10060.1  (AJ012571) glutathione transferase [Arabidopsis thaliana]
GST2_S_AT	GST2	13264_s_at	emb CAA72973.1  (Y12295) glutathione transferase [Arabidopsis thaliana]
GST8_S_AT	GST8	13267_s_at	emb CAA10060.1  (AJ012571) glutathione transferase [Arabidopsis thaliana]
HSC701_S_AT	HSC701	13269_s_at	emb CAA54419.1  (X77199) heat shock cognate 70-1 [Arabidopsis thaliana]
IAA16_S_AT	IAA16	13294_s_at	gb AAB84353.1  (U49072) IAA16 [Arabidopsis thaliana]
IAA8_S_AT	IAA8	13663_s_at	gb AAD15575.1  (AC006340) auxin-regulated protein (IAA8) [Arabidopsis thaliana]
J05216.2_S_AT	J05216.2	16985_s_at	gb AAA32866.1  (J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]
L09755.2_S_AT	L09755.2	19682_s_at	gb AAA32862.1  (L09755) ribosomal protein S28 [Arabidopsis thaliana]
L14844_3_S_AT	L14844	12824_s_at	No hits found less than or equal to 1e-15.
L15389_S_AT	L15389	18679_s_at	No hits found.

Gene ID	Accession # on chip	Affy #	Description
L26984_S_AT	L26984	18682_s_at	gblAAC27463.1  (AC003672) putative small GTP-binding protein [Arabidopsis thaliana]
M21415.4_AT	M21415.4	15988_at	gblAAA32757.1  (M21415) beta-tubulin [Arabidopsis thaliana]
M55077.2_AT	M55077.2	15993_at	gblAAA32868.1  (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]
M64116_3_S_AT	M64116	12827_s_at	gblAAA32794.1  (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase (GapC) [Arabidopsis thaliana]
M84703.2_AT	M84703.2	16480_at	gblAAA32884.1  (M84703) beta-6 tubulin [Arabidopsis thaliana]
ORYZAIN4_AT	ORYZAIN4	14245_at	dbj BAA02374.1  (D13043) thiol protease [Arabidopsis thaliana]
ORYZAIN5_AT	ORYZAIN5	14246_at	emblCAA68192.1  (X99936) cysteine protease [Zea mays]
PHYA_AT	PHYA	14622_at	emblCAA35221.1  (X17341) phyA photoreceptor [Arabidopsis thaliana]
RAN1_S_AT	RAN1	14641_s_at	gblAAD29109.1 AF082565_1 (AF082565) ATP dependent copper transporter [Arabidopsis thaliana]
RD19A_S_AT	RD19A	14644_s_at	emblCAB38829.1  (AL035679) drought-inducible cysteine proteinase RD19A precursor
S69727.2_AT	S69727.2	16503_at	gblAAB20558.1  (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa]
THIOLPROTEASE1_S_AT	THIOLPROTEASE1	14658_s_at	emblCAB38829.1  (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
THIOLPROTEASE3_S_AT	THIOLPROTEASE3	14659_s_at	emb CAB38829.1  (AL035679) drought-inducible cysteine proteinase RD19A precursor
TONOL_F_AT	TONOL	14662_f_at	emb CAA38633.1  (X54854) possible membrane channel protein [Arabidopsis thaliana]
U11256.2_AT	U11256.2	16035_at	gb AAA82212.1  (U11256) metallothionein [Arabidopsis thaliana]
U15108.2_S_AT	U15108.2	16010_s_at	gb AAA50250.1  (U15108) metallothionein-like protein [Arabidopsis thaliana]
U20347.2_S_AT	U20347.2	18651_s_at	gb AAA91976.1  (U20347) mRNA corresponding to this gene accumulates in response to
U21214_S_AT	U21214	18687_s_at	gb AAA86507.1  (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
U33014.2_S_AT	U33014.2	15955_s_at	gb AAB53929.1  (U33014) polyubiquitin [Arabidopsis thaliana]
U35640.2_S_AT	U35640.2	16032_s_at	gb AAC49351.1  (U35640) thioredoxin h [Arabidopsis thaliana]
U35826.2_S_AT	U35826.2	19654_s_at	gb AAC49353.1  (U35826) thioredoxin h [Arabidopsis thaliana]
U41998.4_AT	U41998.4	16476_at	gb AAB37098.1  (U41998) actin 2 [Arabidopsis thaliana]
U43224_S_AT	U43224	12842_s_at	No hits found less than or equal to 1e-15.
U63815.18_S_AT	U63815.18	16429_s_at	gb AAB07880.1  (U63815) ascorbate peroxidase [Arabidopsis thaliana]
U64912.1_S_AT	U64912.1	18989_s_at	gb AAB86892.1  (AF032883) AtJ3 [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
U65471_AT	U65471	18692_at	No hits found less than or equal to 1e-15.
U84969_3_F_AT	U84969	12833_f_at	gblAAB95252.1  (U84969) ubiquitin [Arabidopsis thaliana]
U95973.108_AT	U95973.108	18639_at	gblAAB65482.1  (U95973) endomembrane protein EMP70 precursor isolog [Arabidopsis thaliana]
WT108A_RC_AT	WT108A	14690_at	No hits found less than or equal to 1e-15.
WT755_S_AT	WT755	14701_s_at	emblCAA52237.1  (X74140) RCI14A [Arabidopsis thaliana]
WT758_AT	WT758	14703_at	gblAAD46040.1 AC007519_25 (AC007519) ESTs gblH36253 and gblAA04251 come from this gene. [Arabidopsis thaliana]
X15550_S_AT	X15550	12843_s_at	gblAAD26488.1 AC007195_2 (AC007195) unknown protein [Arabidopsis thaliana]
X16432.2_S_AT	X16432.2	15992_s_at	emblCAA34456.1  (X16432) elongation factor 1-alpha [Arabidopsis thaliana]
X52256.2_AT	X52256.2	16443_at	emblCAB45802.2  (AL080253) translation elongation factor EF-Tu precursor, chloroplast [Arabidopsis thaliana]
X65052_AT	X65052	16026_at	emblCAA46188.1  (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]
X65549.1_AT	X65549.1	15963_at	emblCAA46518.1  (X65549) adenylate translocator [Arabidopsis thaliana]
X68150.1_AT	X68150.1	16451_at	emblCAA48253.1  (X68150) ketol-acid reductoisomerase [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
X69294.2_S_AT	X69294.2	16030_s_at	emb CAA49155.1  (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]
X74604.2_S_AT	X74604.2	15953_s_at	emb CAA52684.1  (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]
X74733.2_AT	X74733.2	16463_at	emb CAA52751.1  (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]
X75162.2_AT	X75162.2	16997_at	emb CAA53005.1  (X75162) BBC1 protein [Arabidopsis thaliana] thaliana]
X75881.2_AT	X75881.2	16446_at	emb CAA53475.1  (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]
X75883.2_AT	X75883.2	15989_at	emb CAB67649.1  (AL132966) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]
X78584.2_AT	X78584.2	16456_at	emb CAA55321.1  (X78584) Di19 [Arabidopsis thaliana]
X81697.2_S_AT	X81697.2	16918_s_at	emb CAA57343.1  (X81697) cysteine synthase [Arabidopsis thaliana]
X82002.1_AT	X82002.1	20261_at	emb CAA57528.1  (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]
X84078_AT	X84078	18710_at	emb CAA58887.1  (X84078) NADH dehydrogenase [Arabidopsis thaliana]
X84315.8_AT	X84315.8	18659_at	No hits found less than or equal to 1e-15.
X84318_AT	X84318	18711_at	emb CAA59061.1  (X84318) NADH dehydrogenase [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
X86962.3_AT	X86962.3	19917_at	emblCAA60525.1  (X86962) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
X91398.2_AT	X91398.2	16988_at	emblCAA62744.1  (X91398) transcription factor L2 [Arabidopsis thaliana]
X91958.1_AT	X91958.1	16469_at	emblCAA63024.1  (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
X91959.1_AT	X91959.1	15890_at	gb AAAF04877.1 AC010796_13 (AC010796) 60S ribosomal protein L27A [Arabidopsis thaliana]
X92510.2_S_AT	X92510.2	19706_s_at	emblCAA63266.1  (X92510) allene oxide synthase [Arabidopsis thaliana]
X94626.1_AT	X94626.1	16508_at	emblCAA64329.1  (X94626) AATP2 [Arabidopsis thaliana]
X99609.2_S_AT	X99609.2	17430_s_at	emblCAA67923.1  (X99609) ubiquitin-like protein [Arabidopsis thaliana]
Y07765.7_S_AT	Y07765.7	16437_s_at	No hits found less than or equal to 1e-15.
Y09482.2_I_AT	Y09482.2	16036_i_at	emblCAA70691.1  (Y09482) HMG1 [Arabidopsis thaliana]
Y10157.3_S_AT	Y10157.3	19833_s_at	emblCAA71239.1  (Y10157) sulfite reductase [Arabidopsis thaliana]
Y10863.1_I_AT	Y10863.1	19919_i_at	emblCAA71879.1  (Y10986) hypothetical protein 194 [Arabidopsis thaliana]
Y12295.2_S_AT	Y12295.2	16033_s_at	emblCAA72973.1  (Y12295) glutathione transferase [Arabidopsis thaliana]
Y14052.2_AT	Y14052.2	16506_at	emblCAA74381.1  (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Gene ID	Accession # on chip	Affy #	Description
Y17053.2_AT	Y17053.2	15960_at	emblCAA76606.1  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
Z12024_AT	Z12024	18731_at	emblCAA78059.1  (Z12024) calmodulin [Arabidopsis thaliana]
Z14989.5_AT	Z14989.5	17414_at	emblCAA78713.1  (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]
Z15157.1_AT	Z15157.1	16982_at	emblCAA78856.1  (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]
Z28702.2_AT	Z28702.2	16984_at	emblCAA82273.1  (Z28701) S18 ribosomal protein [Arabidopsis thaliana]
Z97335.5_S_AT	Z97335.5	16504_s_at	emblCAB10172.1  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Z97336.1_AT	Z97336.1	16930_at	emblCAB10211.1  (Z97336) ribosomal protein [Arabidopsis thaliana]
Z97337.298_S_AT	Z97337.298	16934_s_at	emblCAB10279.1  (Z97337) ribosomal protein [Arabidopsis thaliana]
Z97340.298_S_AT	Z97340.298	15972_s_at	emblCAB10398.1  (Z97340) cysteine proteinase like protein [Arabidopsis thaliana]
Z97341.130_AT	Z97341.130	18230_at	emblCAB10428.1  (Z97341) symbiosis-related like protein [Arabidopsis thaliana]
Z97341.407_AT	Z97341.407	18614_at	emblCAB10447.1  (Z97341) ribosomal protein [Arabidopsis thaliana]
Z97343.270_S_AT	Z97343.270	16926_s_at	emblCAB10520.1  (Z97343) ribosomal protein [Arabidopsis thaliana]



Gene ID	Accession # on chip	Affy #	Description
Z99708.65_AT	Z99708.65	19139_at	emblCAB16820.1  (Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Table 12 provides a description of *Arabidopsis* genes for sequences which are expressed in a leaf-specific manner.

Table 12:

<b>Affy ID</b>	<b>Accession</b>	<b>function</b>	<b>Description</b>
11994_at	AC004218.86_AT	novel	gblAAC27838.1l (AC004218) unknown protein [Arabidopsis thaliana]
12086_s_at	AC002409.88_S_AT	novel	gblAAB86456.1l (AC002409) unknown protein [Arabidopsis thaliana]
12095_at	AC006223.95_AT	novel	gblAAD15394.1l (AC006223) hypothetical protein [Arabidopsis thaliana]
12105_at	AF000657.30_AT	novel	gblAAB72170.1l (AF000657) hypothetical protein [Arabidopsis thaliana]
12115_at	AL033545.26_AT	metabolism	emblCAA22152.1l (AL033545) extensin-like protein [Arabidopsis thaliana]
12135_at	AC007230.29_AT	novel	gblAAD26875.1lAC007230_9 (AC007230) ESTs gblH76289 and gblH76537 come from this gene. [Arabidopsis thaliana]
12270_at	AL030978.79_AT	kinase	emblCAA19724.1l (AL030978) putative receptor protein kinase [Arabidopsis thaliana]
12299_at	AL022347.265_AT	kinase	emblCAA18476.1l (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
12305_i_at	AL022347.219_I_AT	novel	emblCAA18473.1l (AL022347) putative protein [Arabidopsis thaliana]
12392_at	AC002391.102_AT	transcription	gblAAB87103.1l (AC002391) putative MYB family transcription factor [Arabidopsis thaliana]

Affy ID	Accession	function	Description
12788_at	AC002311.20_AT	defense	"gblAAC00607.1l (AC002311) similar to ripening-induced protein, gplAJ001449l2465015 and major#latex protein, gplX91961l1107495 [Arabidopsis thaliana]"
13243_r_at	ELI32_R_AT	metabolism	emblCAB37539.1l (AL035538) cinnamyl-alcohol dehydrogenase ELI3-2 [Arabidopsis
13352_at	AL030978.126_AT	novel	emblCAA19730.1l (AL030978) putative protein [Arabidopsis thaliana]
13620_at	AL035605.41_AT	metabolism	emblCAB38295.1l (AL035605) formamidase-like protein [Arabidopsis thaliana]
13719_at	NOVARTIS106_AT	novel	No hits found less than or equal to 1e-15.
13812_s_at	AC005275.104_S_AT	hormone	gblAAD14468.1l (AC005275) putative GH3-like protein [Arabidopsis thaliana]
13972_s_at	Z97344.134_S_AT	transcription	emblCAB10561.1l (Z97344) SUPERMAN like protein [Arabidopsis thaliana]
14192_at	NOVARTIS66_AT	novel	gblAAC34331.1l (AC004122) Unknown protein [Arabidopsis thaliana]
14218_at	NOVARTIS87_AT	novel	No hits found less than or equal to 1e-15.
14242_s_at	NRA_S_AT	metabolism	gblAAF19225.1lAC007505_1 (AC007505) nitrate reductase [Arabidopsis thaliana]

Affy ID	Accession	function	Description
14248_at	PAD3_AT	metabolism	"gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene."
14432_at	AL035440.502_AT	novel	emb CAB36549.1  (AL035440) putative protein [Arabidopsis thaliana]
14484_at	U73462.2_AT	metabolism	gb AAC32523.1  (U73462) carbonic anhydrase [Arabidopsis thaliana]
14533_i_at	AC007048.166_I_AT	novel	gb AAC32523.1  (U73462) carbonic anhydrase [Arabidopsis thaliana]
14600_at	AC007576.49_AT	novel	gb AAD39297.1 AC007576_20 (AC007576) Unknown protein [Arabidopsis thaliana]
14603_at	AL022347.282_AT	kinase	emb CAA18477.1  (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
14621_at	PDF1.2_AT	defense	gb AAC31244.1  (AC004747) putative antifungal protein [Arabidopsis thaliana]
14635_s_at	PR.1_S_AT	defense	gb AAC69381.1  (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
14682_i_at	WT1012A_RC_I_AT	novel	No hits found.
14709_at	WT788_AT	novel	No hits found less than or equal to 1e-15.

Affy ID	Accession	function	Description
14803_at	AC006550.33_AT	metabolism	gblAAD25807.1 AC006550_15 (AC006550) Strong similarity to gblZ49699 glutaredoxin from Ricinus communis. [Arabidopsis thaliana]
14808_i_at	AC007230.21_I_AT	kinase	gblAAD26873.1 AC007230_7 (AC007230) Contains PF00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]
14862_at	AC005770.205_AT	transcription	gblAAC79620.1  (AC005770) putative RING zinc finger protein [Arabidopsis thaliana]
15185_s_at	AB024283_S_AT	metabolism	dbj BAA78561.1  (AB024283) cysteine synthase [Arabidopsis thaliana]
15271_at	AC004077.141_AT	novel	gblAAC26689.1  (AC004077) unknown protein [Arabidopsis thaliana]
15422_at	AF069441.29_AT	novel	gblAAD36948.1 AF069441_8 (AF069441) hypothetical protein [Arabidopsis thaliana]
15467_at	AC000375.34_AT	novel	gblAAB60770.1  (AC000375) EST gblH37044 comes from this gene. [Arabidopsis thaliana]
15552_at	AL096859.162_AT	novel	emblCAB51187.1  (AL096859) putative protein [Arabidopsis thaliana]
15613_s_at	ATHHOMEOA_S_AT	metabolism	emblCAA79670.1  (Z19602) HAT4 [Arabidopsis thaliana]
15837_at	AC005496.175_AT	metabolism	gblAAC35232.1  (AC005496) putative thiamin biosynthesis protein [Arabidopsis thaliana]
16137_s_at	AF149053_S_AT	metabolism	gblAAD38033.1 AF149053_1 (AF149053) phytochrome kinase substrate 1 [Arabidopsis thaliana]
16172_s_at	D78603_S_AT	metabolism	dbj BAA28535.1  (D78603) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Affy ID	Accession	function	Description
16322_at	AL096860.203_AT	novel	emblCAB51215.1  (AL096860) putative protein [Arabidopsis thaliana]
16323_at	AC005957.35_AT	defense	gblAAD03365.1  (AC005957) putative disease resistance protein [Arabidopsis thaliana]
16331_at	AC005957.23_AT	defense	gblAAD03361.1  (AC005957) putative disease resistance protein [Arabidopsis thaliana]
16365_at	AC003974.136_AT	defense	gblAAC04495.1  (AC003974) putative disease resistance protein [Arabidopsis thaliana]
16547_s_at	AF053941_S_AT	metabolism	gblAAC27293.2  (AF053941) non phototropic hypocotyl 1-like [Arabidopsis thaliana]
16583_s_at	ATHZFPH_S_AT	transcription	gblAAA87304.1  (L39651) zinc finger protein [Arabidopsis thaliana]
16687_s_at	AC004044.64_S_AT	novel	gblAAC79114.1  (AF069442) hypothetical protein [Arabidopsis thaliana]
16845_at	AC006232.87_AT	metabolism	gblAAD15594.1  (AC006232) putative cysteine proteinase [Arabidopsis thaliana]
16856_i_at	AC004681.86_I_AT	metabolism	gblAAC25936.1  (AC004681) putative cellulose synthase [Arabidopsis thaliana]
17019_s_at	ATU28422_S_AT	transcription	gblAAC33507.1  (AC005310) MYB-related transcription factor (CCA1) [Arabidopsis thaliana]
17128_s_at	ATHRPRP1A_S_AT	defense	gblAAC69381.1  (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17231_at	AC004411.170_AT	novel	gblAAC34226.1  (AC004411) hypothetical protein [Arabidopsis thaliana]

Affy ID	Accession	function	Description
17331_at	AF069298.23_AT	kinase	"gblAAC19274.1  (AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabi
17361_s_at	AF096373.28_S_AT	metabolism	emblCAB39764.1  (AL049487) sucrose-phosphate synthase-like protein [Arabidopsis thaliana]
17411_s_at	X98926.1_S_AT	defense	emblCAA67426.1  (X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis thaliana]
17815_s_at	Z97342.284_S_AT	defense	emblCAB46050.1  (Z97342) disease resistance RPP5 like protein (fragment) [Arabidopsis thaliana]
17835_at	AF096370.14_AT	RNA binding protein	gblAAC62779.1  (AF096370) contains similarity to Arabidopsis thaliana reverse transcriptase-like proteins
17861_s_at	AC005560.16_S_AT	transport	gblAAC67319.1  (AC005560) putative auxin transport protein [Arabidopsis thaliana]
17936_s_at	Z97342.384_S_AT	metabolism	emblCAB46051.1  (Z97342) putative beta-amylase [Arabidopsis thaliana]
18115_at	AC005388.43_AT	kinase	gblAAC64891.1  (AC005388) Similar to T11J7.13 gil2880051 putative protein kinase from Arabidopsis thaliana BAC gblAC002340.
18296_at	AC002510.60_AT	kinase	gblAAB84338.1  (AC002510) putative Ca <sup>2+</sup> -ATPase [Arabidopsis thaliana]

Affy ID	Accession	function	Description
18301_s_at	AL022223.48_S_AT	metabolism	emblCAA18218.1  (AL022223) fructose-bisphosphate aldolase [Arabidopsis thaliana]
18469_at	AC006341.12_AT	kinase	gblAAD34678.1 AC006341_6 (AC006341) Similar to gblAJ012423 wall-associated kinase 2 from Arabidopsis thaliana.
18588_at	AL022604.205_AT	novel	emblCAA18744.1  (AL022604) putative protein [Arabidopsis thaliana]
18670_g_at	AJ250341_G_AT	metabolism	emblCAB58423.1  (AJ250341) beta-amylase enzyme [Arabidopsis thaliana]
18778_at	Z97338.384_AT	novel	emblCAB10322.1  (Z97338) hypothetical protein [Arabidopsis thaliana]
18811_at	AC002396.32_AT	novel	gblAAC00583.1  (AC002396) Hypothetical protein [Arabidopsis thaliana]
18835_at	AC007260.34_AT	novel	gblAAD30584.1 AC007260_15 (AC007260) lclprt_seq No definition line found [Arabidopsis thaliana]
18844_at	AC005315.131_AT	transport	gblAAC33239.1  (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
18866_at	AC005917.178_AT	transposable element	gblAAD10163.1  (AC005917) putative Ta11-like non-LTR retroelement protein [Arabidopsis thaliana]
19034_at	AL021768.117_AT	defense	emblCAA16930.1  (AL021768) TMV resistance protein N-like [Arabidopsis thaliana]
19465_at	AL021768.96_AT	defense	emblCAA16929.1  (AL021768) resistance protein RPP5-like [Arabidopsis thaliana]



Affy ID	Accession	function	Description
19581_at	AC006526.102_AT	transport	gblAAD23055.1 AC006526_14 (AC006526) putative cyclic nucleotide-regulated ion channel protein [Arabidopsis thaliana]
19704_i_at	AJ005927.2_I_AT	metabolism	emblCAA06769.1  (AJ005927) squalene epoxidase homologue [Arabidopsis thaliana]
19718_at	AC000098.16_AT	transport	gblAAB71447.1  (AC000098) Similar to Arabidopsis Fe(II) transport protein (gblU27590). [Arabidopsis thaliana]
19720_at	AC003979.28_AT	hormone	gblAAC25517.1  (AC003979) Contains similarity to gibberellin-regulated protein 2 precursor (GAST1) homolog gblU11765 from A. thaliana. [Arabidopsis thaliana]
19774_at	AC007167.248_AT	transport	gblAAD30549.1 AF136580_1 (AF136580) iron-regulated transporter 2 [Lycopersicon esculentum]
19834_at	AC006264.14_AT	hormone	gblAAD29795.1 AC006264_3 (AC006264) putative auxin-regulated protein [Arabidopsis thaliana]
19889_at	AC003033.139_AT	novel	gblAAB91986.1  (AC003033) unknown protein [Arabidopsis thaliana]
19901_at	AC003033.129_AT	novel	gblAAB91985.1  (AC003033) unknown protein [Arabidopsis thaliana]
19992_at	AC007138.58_AT	novel	gblAAD22657.1 AC007138_21 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
20062_at	AC005896.23_AT	novel	gblAAC98045.1  (AC005896) unknown protein [Arabidopsis thaliana]

Affy ID	Accession	function	Description
20063_at	AC006284.5_AT	metabolism	gblAAD17422.1l (AC006284) putative esterase [Arabidopsis thaliana]
20232_s_at	AL022347.12_S_AT	kinase	emblCAA18460.1l (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20356_at	AC004561.74_AT	metabolism	gblAAC95191.1l (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
20429_s_at	Z97336.167_S_AT	novel	emblCAB10219.1l (Z97336) hypothetical protei [Arabidopsis thaliana]
20525_at	AC007169.89_AT	transcription	gblAAD26481.1lAC007169_13 (AC007169) putative CONSTANS-like B-box zinc finger protein [Arabidopsis thaliana]
20537_at	AL049608.65_AT	metabolism	emblCAB40769.1l (AL049608) extensin-like protein [Arabidopsis thaliana]
20544_at	AL035679.68_AT	transcription	emblCAB38816.1l (AL035679) putative zinc finger protein [Arabidopsis thaliana]
20705_at	AL049607.66_AT	metabolism	emblCAB40757.1l (AL049607) glutathione peroxidase-like protein [Arabidopsis thaliana]

Table 13 provides cumulative sequence identifier numbers for the SEQ ID Nos disclosed in the sequence listing. NOTE: please refer to cross referenced SEQ ID NOs Table since a single SYNGENTA NO: may refer to more than one SEQ ID NO.

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Table 13:

SEQ ID NOs 1-773 and their corresponding reference numbers

SEQ ID NO:	SYNGENTA NO:
<b>Root promoter reference numbers from the provisional application US 60/214087</b>	
1	AC006592.51
2	A71588.1
3	A71596.1
4	AC001645.19
5	AC001645.47
6	AC001645.50
7	AC002333.199
8	AC002333.210
9	AC002391.150
10	AC003673.201
11	AC004005.104
12	AC004521.114
13	AC004521.119
14	AC004683.79
15	AC004684.165
16	AC005310.6

SEQ ID NO:	SYNGENTA NO:
17	AC005560.136
18	AC005560.147
19	AC005967.50
20	AC006216.22
21	AC006216.26
22	AC006577.16
23	AC006587.164
24	AC007060.34
25	AC007135.23
26	AC007584.48
27	ACHI
28	AF098630.3
29	AF128395.12
30	AL035538.245
31	AL049500.57
32	AL049638.193
33	AL049730.104
34	AL080253.32
35	AL080282.74
36	ATAJ2596
37	ATHORF
38	ATPIN2
39	ATU10034

SEQ ID NO:	SYNGENTA NO:
40	ATU57320
41	ATU62330
42	CAFFEROYL
43	NOVARTIS51
44	U72155.2
45	U81294.2
46	X98319.2
47	X98855.2
48	Z97338.321
49	Z97340.345
50	Z97344.151
51	Z99707.288
<b>Constitutive promoter reference numbers from the provisional application US 60/213848</b>	
52	AC003981.34
53	AC004557.8
54	AC005287.52
55	AC006085.15
56	AC007138.25
57	AC007576.5
58	AC007659.93
59	AF013959.4
60	AF0027172.3

SEQ ID NO:	SYNGENTA NO:
61	AF0083337.3
62	AF0123253.3
63	AC002332.71
64	AC002334.110
65	AC002336.101
66	AC002339.51
67	AC002521.146
68	AC002561.51
69	AC003672.64
70	AC004077.166
71	AC004165.105
72	AC004218.83
73	AC004401.140
74	AC004450.83
75	AC004481.84
76	AC004665.31
77	AC004669.34
78	AC004747.160
79	AC005169.221
80	AC005309.64
81	AC005397.40
82	AC005662.30
83	AC005727.191

SEQ ID NO:	SYNGENTA NO:
84	AC005824.21
85	AC005896.150
86	AC005897.156
87	AC005936.95
88	AC006068.93
89	AC006200.119
90	AC006201.107
91	AC006223.65
92	AC006234.156
93	AC006260.52
94	AC006264.30
95	AC006300.70
96	AC006403.110
97	AC006526.57
98	AC006532.47
99	AC006585.146
100	AC006586.141
101	AC006841.122
102	AC006919.171
103	AC006921.52
104	AC006929.77
105	AC006951.208
106	AC007017.278

SEQ ID NO:	SYNGENTA NO:
107	AC007019.105
108	AC007070.167
109	AC007071.72
110	AC007119.88
111	AC007135.50
112	AC007170.48
113	AC007195.93
114	AF000657.40
115	Z99708.65
116	AL035440.66
117	AL021811.156
118	AL021636.178
119	AL049480.178
120	AL031326.138
121	AL035679.232
122	AL022224.72
123	AL035540.94
124	AL035356.123
125	AL050300.27
126	AL022141.10
127	AL035526.101
128	AL078464.37
129	AL034567.189



SEQ ID NO:	SYNGENTA NO:
130	AL035394.117
131	Z97335.5
132	Z97336.1
133	Z97337.298
134	Z97340.298
135	Z97341.407
136	Z97343.270
137	X84315.8
138	D13043.4
139	AL050398.4
140	AL022023.145
141	Y10157.3
142	AL021712.156
143	AL021687.199
144	AL022373.153
145	AL078637.47
146	AL035680.53
147	AL049171.25
148	AL035709.87
149	AL078468.11
150	AL023094.323
151	AL022580.188
152	AL021890.209

SEQ ID NO:	SYNGENTA NO:
153	AL035656.126
154	AL049608.184
155	U33014.2
156	U41998.4
157	U63815.18
158	U95973.108
159	A45785.1
160	AB003522.2
161	AB004872.6
162	AB005560
163	AB006693.1
164	AB008105
165	AB008487
166	AB010946
167	AB011545
168	AB017643
169	AB021858
170	AB024282
171	AB027151.2
172	AC000103.25
173	AC000104.10
174	AC000104.26
175	AC000132.16

SEQ ID NO:	SYNGENTA NO:
176	AC000132.6
177	AC002131.48
178	AC002329.46
179	AC002330.39
180	AC002332.100
181	AC002332.71
182	AC002334.110
183	AC002336.101
184	AC002339.51
185	AC002343.3
186	AC004165.105
187	AC004401.140
188	AC004481.84
189	AC006438.21
190	AC006922.106
191	AF001394
192	AF003096
193	AF003105.1
194	AF004216
195	AF004393
196	AF017641
197	AF027174
198	AF034387

SEQ ID NO:	SYNGENTA NO:
199	AF034694
200	AF043519
201	AF043528
202	AF044265
203	AF044313
204	AF059294
205	AF061519
206	AF063901
207	AF074375
208	AF076484
209	AF076641
210	AF077528
211	AF082565
212	AF118822
213	AF136152
214	AF144387
215	AF167983
216	AF181688
217	AF181966
218	AF186847
219	AGO1
220	AJ001397
221	AJ010505

SEQ ID NO:	SYNGENTA NO:
222	AJ011628
223	AJ131205
224	AL096856
225	AL096860
226	AOS
227	APX3
228	ATADH111
229	ATERF3
230	ATHADPRFA
231	ATHAVAP
232	ATHAVAPA
233	ATHDYNAGTP
234	ATHERD13
235	ATHERD15
236	ATHGFPSIA
237	ATHHMGCOAR
238	ATHMERI5B
239	ATHMTMACP
240	ATHPRPHC
241	ATHRPCA
242	ATHSAR1
243	ATORNCARB
244	ATTHIRED2

SEQ ID NO:	SYNGENTA NO:
245	ATTHIRED3
246	ATU01955
247	ATU15108
248	ATU15130
249	ATU18410
250	ATU18675
251	ATU20347
252	ATU21214
253	ATU22340
254	ATU36765
255	ATU37235
256	ATU37281
257	ATU37587
258	ATU39485
259	ATU43325
260	ATU43397
261	ATU46665
262	ATU49072
263	ATU49259
264	ATU52851
265	ATU56929
266	ATU63633
267	ATU66343

SEQ ID NO:	SYNGENTA NO:
268	ATU68545
269	ATU75191
270	ATU77381
271	ATU78297
272	ATU78870
273	ATU79960
274	ATU80186
275	ATU91995
276	CATL
277	CYSPROL
278	D01027.1
279	D11394.2
280	D83531
281	GLUTATHIONEPEROXIDASE
282	GST1
283	GST2
284	HSC701
285	IAA16
286	IAA8
287	J05216
288	L09755.2
289	L14844.3
290	L15389

SEQ ID NO:	SYNGENTA NO:
291	L26984
292	M55077.2
293	M64116
294	ORYZAIN4
295	ORYZAIN5
296	PHYA
297	RAN1
298	RD19A
299	THIOLPROTEASE1
300	TONOL
301	U11256.2
302	U15108.2
303	U20347
304	U21214
305	U35826.2
306	U64912.1
307	WT755
308	X16432
309	X68150.1
310	X74604.2
311	X74733.2
312	X75162
313	X75881



SEQ ID NO:	SYNGENTA NO:
314	X75883.2
315	X81697.2
316	X84078
317	X84318
318	X91398
319	X91959.1
320	X99609
321	Y07765.7
322	Y12295
323	Y12295.2
324	Y14052
325	Y17053.2
326	Z12024
327	Z15157.1
328	AC002131.48
329	AC006577.32
330	AC000104.26
331	AC000132.6
332	AF080120.11
333	AC007357.17
334	AC005990.10
335	AF069299.19
336	AC000106.13

SEQ ID NO:	SYNGENTA NO:
337	AC005679.10
338	AC004393.22
339	AC005388.6
<b>Root primers</b>	
340	ARF1
341	ARR1
342	ARF2
343	ARR2
344	ARF5
345	ARR5
346	ARF6
347	ARR6
348	ARF8
349	ARR8
350	ARF9
351	ARR9
352	ARF10
353	ARR10
354	ARF11
355	ARR11
356	ARF13
357	ARR13
<b>Root ORFs</b>	

SEQ ID NO:	SYNGENTA NO:
358	AC001645.19
359	AC002333.199
360	AC002333.210
361	AC007135.23
362	AFO98630.3
363	AL035538.245
364	AL080253.32
365	X98855.2
366	Z97338.321
<b>Constitutive primers</b>	
367	ACF1
368	ACR1
369	ACF2
370	ACR2
371	ACF3
372	ACR3
373	ACF4
374	ACR4
375	ACF6
376	ACR6
377	ACF7
378	ACR7
379	ACF8

SEQ ID NO:	SYNGENTA NO:
380	ACR8
381	ACF9
382	ACR9
383	ACF10
384	ACR10
385	ACF11
386	ACR11
387	ACF12
388	ACR12
389	ACF13
390	ACR13
391	ACF14
392	ACR14
393	ACF15
394	ACR15
395	ACF16
396	ACR16
397	ACF19
398	ACR19
399	ACF20
400	ACR20
401	ACF21
402	ACR21

SEQ ID NO:	SYNGENTA NO:
403	ACF22
404	ACR22
405	ACF23
406	ACR23
407	ACF24
408	ACR24
409	ACF25
410	ACR25
411	ACF26
412	ACR26
413	ACF27
414	ACR27
415	ACF31
416	ACR31
417	ACF32
418	ACR32
419	ACF34
420	ACR34
421	ACF35
422	ACR35
423	ACF38
424	ACR38
425	ACF39

SEQ ID NO:	SYNGENTA NO:
426	ACR39
427	ACF40
428	ACR40
429	ACF41
430	ACR41
431	ACF42
432	ACR42
433	ACF44
434	ACR44
435	ACF45
436	ACR45
437	ACF46
438	ACR46
439	ACF47
440	ACR47
<b>Constitutive ORFs</b>	
441	WT755
442	AF004393
443	ATU46665
444	D83531
445	AB017643
446	ATU56929
447	AB005560

SEQ ID NO:	SYNGENTA NO:
448	AC006438.21
449	AC002131.48
450	AC007138.25
451	AL049608.184
452	AC006264.30
453	AL022224.72
454	AC005897.156
455	AL021890.14
456	AC006234.156
457	AC006526.57
458	AC004747.160
459	AC005309.201
460	AL021636.178
461	AC003981.34
462	AC005727.191
463	AF080120.11
464	AC006300.112
465	AL035679.13
466	AC007195.93
467	Z1517.1
468	AL035709.87
469	AL035656.126
470	AC006403.110

SEQ ID NO:	SYNGENTA NO:
471	U95973.108
472	AC002561.51
473	AL035440.66
474	AC004557.8
475	AL021712.156
476	Y07765.7
<b>Constitutive promoters</b>	
477	AC000104.26
478	AJ001397
479	L14844
480	AL021890.14
481	AL035679.13
482	AC002561.51
483	AC003981.34
484	AC004557.8
485	AC004747.160
486	AC005727.191
487	AC005897.156
488	AC006234.156
489	AC006264.30
490	AC006403.110
491	AC006526.57
492	AC007138.25



SEQ ID NO:	SYNGENTA NO:
493	AC007195.93
494	AF080120.11
495	AL021636.178
496	AL021712.156
497	AL022224.72
498	AL035440.66
499	AL035656.126
500	AL035709.87
501	AL049608.184
502	AB005560
503	AB017643
504	AC002131.48
505	AC006438.21
506	AF004393
507	ATU46665
508	ATU56929
509	D83531
510	WT755
511	Z15157.1
512	U95973.108
513	Z97340.298
514	AC005309.201
515	AC006300.112

SEQ ID NO:	SYNGENTA NO:
516	-
517	Y07765.7
<b>Root promoters</b>	
518	AC007135.23
519	AF098630.3
520	AL035538.245
521	AL080253.32
522	X98855.2
523	Z97338.321
524	AC001645.19
525	AC002333.199
526	AC002333.210
<b>Constitutive ORFs</b>	
527	L14844.3
528	AJ001397
529	AC000104.26
<b>Constitutive primers</b>	
530	18011 (forward)
531	18011 (reverse)
532	12771 (forward)
533	12771 (reverse)
534	12824 (forward)
535	12824 (reverse)

SEQ ID NO:	SYNGENTA NO:
<b>Cloned root promoters</b>	
536	AC002333.199
537	AC002333.210
538	AC007135.23
539	AL035538.245
540	AL080253.32
541	Z97338
542	AC001645
543	AF098630
544	X98855.2
<b>Cloned constitutive promoters</b>	
545	AC002561
546	AC006234
547	AC006264.30
548	AC006403
549	AC006526.57
550	AC007138
551	AC007195.93
552	AF080120.11
553	AL021636.178
554	AL021712.156
555	AL022224.72
556	AL035440.66

SEQ ID NO:	SYNGENTA NO:
557	AL035656
558	AL035709.87
559	AL049608.184
560	AB005560
561	AB017643
562	AC002131
563	AC006438.21
564	AF004393
565	ATU46665
566	ATU56929
567	Z97340
568	D83531
569	WT755
570	ATU63633
571	Z15157.1
572	AC005727
573	AC005309.201
574	AC006300
575	AL021890
576	AL035679.13
577	AC000104
578	L14844
579	AJ001397

SEQ ID NO:	SYNGENTA NO:
580	-
<b>Sequences from the PCT specification</b>	
581	pNOV2374 binary Gateway destination vector with GIG reporter gene
582	GIG, GUS intron GUS, GUS coding sequence with intron
583	Ubq3(At) Arabidopsis thaliana Ubiquitin 3 promoter plus intron
584	5'- GGCCAGTGAATTGTAATACGACTCACTA TAGGGAGGCGG-(dT)24-3'
585	5'- GGCCAGTGAATTGTAATACGACTCACTA TAGGGAGGCGG-(dT)24-3'
586	5'-TGGTTCGGACC-3'
587	TRX3T 5' 6-FAM agacttcactgcaacatggtgccac TAMRA 3'
588	TRX3F 5' gtgtggaaatgacacagattgtga3'
589	TRX3R 5'agacgggtgcaatgaaacg3'
590	APX3 T 5' 6-FAM cgcgaacaagaactgtgtcctatcatg TAMRA 3'
591	APX3 F 5'gccgtgagctccgttctct3'
592	APX3 R 5'tcgtgccatgccaatcg3'
593	-
594	-

SEQ ID NO:	SYNGENTA NO:
595	-
596	-
597	-
598	DNA for rice ortholog (OS000026)
599	DNA (CDS) for rice ortholog (OS000026)
600	Amino acid for rice ortholog (OS000026)
<b>Leaf ORFs from the provisional application US 60/258692</b>	
601	ELI32
602	Novartis106
603	Novartis66
604	Novartis87
605	NRA
606	PAD3
607	PDF1.2
608	PR.1
609	WT1012A
610	WT788
611	AB024283
612	Athhomeoa
613	Af149053
614	D78603
615	Af053941
616	Athzfph

SEQ ID NO:	SYNGENTA NO:
617	ATU28422
618	athrprpla
619	AJ250341
620	AC002311.20
621	AL035605.41
622	AC007048.166
623	AC007576.49
624	AL022347.282
625	AC000375.34
626	AL096859.162
627	X98926.1
628	AC005560.16
629	Z97342.384
630	AC002510.60
631	AL022223.48
632	AL022604.205
633	AL021768.96
634	AJ005927.2
635	AC006264.14
636	AC003033.139
637	AC003033.129
638	AC007138.58
639	AC005896.23

SEQ ID NO:	SYNGENTA NO:
640	AC006284.5
641	AL022347.12
642	AC004561.74
643	Z97336.167
644	AC007169.89
645	AL049608.65
646	AL035679.68
647	AL049607.66
648	AC004218.86
649	AC002409.88
650	AC006223.95
651	AF000657.30
652	AL033545.26
653	AC007230.29
654	AL030978.79
655	AL022347.265
656	AL022347.219
657	AC002391.102
658	Z97344.134
659	AL035440.502
660	U73462.2
661	AC005770.205
662	AF069441.29



SEQ ID NO:	SYNGENTA NO:
663	AC005496.175
664	AL096860.203
665	AC005957.35
666	AC005957.23
667	AC003974.136
668	AC006232.87
669	AC004681.86
670	AF069298.23
671	AF096373.28
672	Z97342.284
673	AF096370.14
674	AC005388.43
675	AC006341.12
676	Z97338.384
677	AC002396.32
678	AC007260.34
679	AC005315.131
680	AC005917.178
681	AL021768.117
682	AC006526.102
683	AC000098.16
684	AC003979.28
685	AC007167.248

SEQ ID NO:	SYNGENTA NO:
686	AL30978.126
687	AC005275.104
688	AC006550.33
689	AC007230.21
690	AC004077.141
691	AC004044.64
692	AC004411.170
<b>Leaf promoters from the provisional application US 60/258692</b>	
693	ELI32
694	Novartis106
695	NRA
696	PAD3
697	PDF1.2
698	PR.1
699	Athhomeoa
700	AF149053
701	athzfph
702	ATU28422
703	athrprp1a
704	AJ250341
705	AC002311.20
706	AL035605.41
707	AC007576.49

SEQ ID NO:	SYNGENTA NO:
708	AL022347.282
709	AC000375.34
710	AL096859.162
711	X98926.1
712	AC005560.16
713	Z97342.384
714	AC002510.60
715	AL022223.48
716	AL022604.205
717	AL021768.96
718	AC003033.139
719	AC003033.129
720	AC007138.58
721	AC005896.23
722	AC006284.5
723	AL022347.12
724	AC004561.74
725	Z97336.167
726	AC007169.89
727	AL049608.65
728	AL035679.68
729	AL049607.66
730	AC004218.86

SEQ ID NO:	SYNGENTA NO:
731	AC002409.88
732	AC006223.95
733	AF000657.30
734	AL033545.26
735	AC007230.29
736	AL030978.79
737	AL022347.265
738	AL022347.219
739	AC002391.102
740	Z97344.134
741	AL035440.502
742	U73462.2
743	AC005770.205
744	AF069441.29
745	AC005496.175
746	AL096860.203
747	AC005957.35
748	AC005957.23
749	AC003974.136
750	AC006232.87
751	AC004681.86
752	AF069298.23
753	AF096373.28

SEQ ID NO:	SYNGENTA NO:
754	Z97342.284
755	AF096370.14
756	AC005388.43
757	AC006341.12
758	Z97338.384
759	AC002396.32
760	AC007260.34
761	AC005315.131
762	AC005917.178
763	AL021768.117
764	AC006526.102
765	AC000098.16
766	AC003979.28
767	AL30978.126
768	AC005275.104
769	AC006550.33
770	AC007230.21
771	AC004077.141
772	AC004044.64
773	AC004411.170

Table 14 Identification of rice homologs to the Arabidopsis ORFs and their corresponding promoters

The peptide sequences corresponding to the full-length Arabidopsis ORFs are formatted into a BLAST database. Then, a BLASTP comparison search is performed with the Arabidopsis sequences. Since there is no description associated with the predicted protein sequences, the stringency of the SCAN post process is increased. The default parameters of SCAN are set so that all of the results have 60 or more identities and that 60% of the alignment is made up of identities. An  $1e-4$  E-value cutoff is implemented and additionally no more than the top 5 hits are taken. Then the mRNA sequences for these predictions are retrieved and included in the listing along with the 2kb upstream promoter region. A PERL script carries out this process.

Table 14:

Arabidopsis ORF (SEQ ID NO)	Homologous rice ORF (SEQ ID NO)	Promoter of rice gene with homologous ORF (SEQ ID NO)
360	774	825
360	792	843
441	789	840
441	790	841
441	799	850
441	813	864
442	781	832
442	804	855
442	805	856
442	810	861
442	816	867
442	817	868

Arabidopsis ORF (SEQ ID NO)	Homologous rice ORF (SEQ ID NO)	Promoter of rice gene with homologous ORF (SEQ ID NO)
442	822	873
443	777	828
443	782	833
443	783	834
443	806	857
443	820	871
446	791	842
446	793	844
446	808	859
449	795	846
450	776	827
450	784	835
450	787	838
450	800	851
450	807	858
451	779	830
454	803	854
458	788	839
465	786	837

Arabidopsis ORF (SEQ ID NO)	Homologous rice ORF (SEQ ID NO)	Promoter of rice gene with homologous ORF (SEQ ID NO)
466	775	826
466	778	829
466	814	865
466	815	866
467	785	836
467	798	849
471	794	845
471	809	860
471	812	863
472	797	848
527	780	831
527	796	847
527	802	853
527	819	870
527	821	872
527	823	874
528	811	862
528	824	875
529	801	852
529	818	869



## Table 15....Identification of homologous genes

Homologs are identified through the use of BLAST and SCAN software with some additional filters. The simplest way to identify homologs is to perform searches on a protein level. The Arabidopsis sequences referred to in the table below are full length CDS which have an associated peptide sequence. A BLAST database that is a subset of GenBank ver 123.0 (Release Date April 15, 2001) is created that contains all of the Plant translated regions excluding Arabidopsis thaliana sequences. The subset is created with a PERL script. Then, a BLAST search (BLASTP specifically) is performed with all of the peptide sequences of the present invention against the GenBank subset. SCAN (the Sequence Comparison Analysis, program ver 1.0k licensed from the Los Alamos National Laboratories) is then used with its default settings to post-process the BLAST results and to identify homologous sequences. In addition to SCAN, an E-value cutoff of  $\leq 1e-4$  is implemented. Finally, to determine if these sequences could be orthologs, another filter is implemented. This filter takes advantage of the fact that many of the Arabidopsis CDS already have description assigned by TIGR and its collaborators. When the GenBank subset is created, annotation from following fields is retained: product, function, and note (protein and nucleotide accessions and organism are also kept). For each homolog found by SCAN below the E-value cutoff, the words in the description to the text of the annotation are compared. If any of the words match, then the sequence is considered to have the same or similar function. Since many words in the description do not specify function to the following words are eliminated from being used in the comparison.

Excluded Words:

The, like, protein, related, unknown, subunit, hypothetical, and, putative, precursor, clone, homolog, small, beta, class, dna, rna, alpha, gamma, has, not, been, from, to, by, long, type, induced

Table 15:

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
358	CAA72271.1 Y11483 Brassica napus DESCRIPTION: jasmonate inducible protein
359	BAA22966.1 D45182 Chenopodium amaranticolor DESCRIPTION: chitinase
	CAA43708.1 X61488 Brassica napus DESCRIPTION: chitinase
	BAB21377.1 AB054811 Oryza sativa DESCRIPTION: PR-3 class IV chitinase. Cht4. Catalytic domain
	BAB21374.1 AB054687 Oryza sativa DESCRIPTION: PR-3 class IV chitinase. Cht4. catalytic domain
	BAA19793.1 AB003194 Oryza sativa DESCRIPTION: chitinase IIb
	AAB65777.1 U97522 Vitis vinifera DESCRIPTION: class IV endochitinase. VvChi4B
360	CAA43708.1 X61488 Brassica napus DESCRIPTION: chitinase
	AAB65777.1 U97522 Vitis vinifera DESCRIPTION: class IV endochitinase. VvChi4B
	AAB65776.1 U97521 Vitis vinifera DESCRIPTION: class IV endochitinase. VvChi4A
	BAB21377.1 AB054811 Oryza sativa DESCRIPTION: PR-3 class IV chitinase. Cht4. Catalytic domain
	BAB21374.1 AB054687 Oryza sativa DESCRIPTION: PR-3 class IV chitinase. Cht4. catalytic domain
	BAA19793.1 AB003194 Oryza sativa DESCRIPTION: chitinase IIb

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	CAA87072.1 Z46948 Sambucus nigra DESCRIPTION: hydrolyse internal glycosidic linkages of chitin. pathogenesis-related protein PR-3 type
	BAA22966.1 D45182 Chenopodium amaranticolor DESCRIPTION: chitinase
	BAA22965.1 D45181 Chenopodium amaranticolor DESCRIPTION: chitinase
	BAA22968.1 D45184 Chenopodium amaranticolor DESCRIPTION: chitinase
	BAA22967.1 D45183 Chenopodium amaranticolor DESCRIPTION: chitinase
	AAC35981.1 AF090336 Citrus sinensis DESCRIPTION: chitin hydrolase. chitinase CHI1. chi1
	AAA33444.1 M84164 Zea mays DESCRIPTION: chitinase A. seed chitinase
	CAA87074.1 Z46950 Sambucus nigra DESCRIPTION: hydrolyses internal glycosidic linkages of chitin. pathogenesis-related protein, PR-3 type
	CAA53544.1 X75945 Beta vulgaris DESCRIPTION: chitinase. Ch4
	CAA40474.1 X57187 Phaseolus vulgaris DESCRIPTION: chitinase. Chi4
362	BAB16431.1 AB041519 Nicotiana tabacum DESCRIPTION: P-rich protein Nt-SubC29. Nt-SubC29
	BAA11855.1 D83227 Populus nigra DESCRIPTION: extensin like protein
	BAA11854.1 D83226 Populus nigra DESCRIPTION: extensin like protein

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	AAK30571.1 AF346659 Brassica napus DESCRIPTION: extensin-like protein
	AAC60566.1 S68113 Brassica napus DESCRIPTION: proline-rich SAC51. This sequence comes from Fig. 3
365	CAA62228.1 X90695 Medicago sativa DESCRIPTION: peroxidase2. prx2.
	CAA09881.1 AJ011939 Trifolium repens DESCRIPTION: peroxidase. prx2
441	AAC04811.1 AF037460 Fritillaria agrestis DESCRIPTION: GF14 protein. GRF
	AAF76226.1 AF272572 Populus x canescens DESCRIPTION: 14-3-3 protein. 14-3-3P20-1
	AAF05737.1 AF191746 Lilium longiflorum DESCRIPTION: 14-3-3-like protein
	AAC49894.1 U91726 Nicotiana tabacum DESCRIPTION: 14-3-3 isoform e. T14-3e
	AAB40395.1 U80070 Mesembryanthemum crystallinum DESCRIPTION: G-box binding factor. 14-3-3-like protein. GBF
	AAB09580.1 U70533 Glycine max DESCRIPTION: SGF14A. 14-3-3 related protein
	AAB07457.1 U65957 Oryza sativa DESCRIPTION: GF14-c protein. rice 14-3-3 protein homolog; osGF14c
	AAB33304.1 S77133 Zea mays DESCRIPTION: GF14-6. GRF1. 14-3-3 protein homolog; This sequence comes from Fig. 5
	AAA99431.1 L29150 Lycopersicon esculentum

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: 14-3-3 protein homologue
	CAA74592.1 Y14200 Hordeum vulgare DESCRIPTION: 14-3-3 protein
	AAB07456.1 U65956 Oryza sativa DESCRIPTION: GF14-b protein. rice 14-3-3 protein homolog; osGF14b
	AAD27827.2 AF121198 Picea glauca DESCRIPTION: 14-3-3 protein. 14-3-3EB9D
	AAD27823.2 AF121194 Populus x canescens DESCRIPTION: 14-3-3 protein. 14-3-3P20-2
	BAA03711.1 D16140 Oryza sativa DESCRIPTION: brain specific protein. S94
	CAA44259.1 X62388 Hordeum vulgare DESCRIPTION: 14-3-3 protein homologue
	CAA66309.1 X97724 Solanum tuberosum DESCRIPTION: 14-3-3 protein. leaf specific
	CAA63658.1 X93170 Hordeum vulgare DESCRIPTION: Hv14-3-3b.
	AAA85817.1 U15036 Pisum sativum DESCRIPTION: 14-3-3-like protein
	CAB42546.2 AJ238681 Pisum sativum DESCRIPTION: 14-3-3-like protein. 14-3-3
	CAA53700.1 X76086 Cucurbita pepo DESCRIPTION: 14-3-3 protein 32kDa endonuclease. A215. single polypeptide
	AAA33505.1 M96856 Zea mays DESCRIPTION: regulatory protein. GF14-12
	AAK26634.1 AF342780 Brassica napus

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: GF14 omega. 14-3-3 protein
	CAA44642.1 X62838 Oenothera elata subsp. hookeri DESCRIPTION: protein kinase C inhibitor homologue
	CAA72383.1 Y11687 Solanum tuberosum DESCRIPTION: 14-3-3 protein. 34G
	AAC49892.1 U91724 Nicotiana tabacum DESCRIPTION: 14-3-3 isoform c. T14-3c
	CAA72094.1 Y11211 Nicotiana tabacum DESCRIPTION: 14-3-3-like protein B
	CAA72382.1 Y11686 Solanum tuberosum DESCRIPTION: 14-3-3 protein. 30G
	CAB42547.1 AJ238682 Pisum sativum DESCRIPTION: 14-3-3-like protein. 14-3-3
	CAA72381.1 Y11685 Solanum tuberosum DESCRIPTION: 14-3-3 protein. 16R
	AAC49891.1 U91723 Nicotiana tabacum DESCRIPTION: 14-3-3 isoform b. T14-3b
	AAB07458.1 U65958 Oryza sativa DESCRIPTION: GF14-d protein. rice 14-3-3 protein homolog; osGF14d
	BAB11739.1 AB042193 Triticum aestivum DESCRIPTION: TaWIN1. TaWIN1. TaWIN1 is a member of 14- 3-3 protein family
	AAC49895.1 U91727 Nicotiana tabacum DESCRIPTION: 14-3-3 isoform f. T14-3f
	CAA65147.1 X95902 Lycopersicon esculentum DESCRIPTION: 14-3-3 protein. tft3 gene
	CAA65146.1 X95901 Lycopersicon esculentum

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: 14-3-3 protein. tft2 gene
	CAB65693.1 AJ270959 Lycopersicon esculentum DESCRIPTION: tft3 14-3-3 protein. tft3
	AAC17447.1 AF066076 Helianthus annuus DESCRIPTION: 14-3-3-like protein
	CAA72095.1 Y11212 Nicotiana tabacum DESCRIPTION: 14-3-3-like protein A
	CAA65148.1 X95903 Lycopersicon esculentum DESCRIPTION: 14-3-3 protein. tft5 gene
	CAC03467.1 Y19105 Chlamydomonas reinhardtii DESCRIPTION: 14-3-3 protein
	CAA55964.1 X79445 Chlamydomonas reinhardtii DESCRIPTION: 14-3-3 protein
	CAA60800.1 X87370 Solanum tuberosum DESCRIPTION: 14-3-3 protein. RA215. root specific
	CAA65149.1 X95904 Lycopersicon esculentum DESCRIPTION: 14-3-3 protein. tft6 gene
	BAB11740.1 AB042194 Triticum aestivum DESCRIPTION: TaWIN2. TaWIN2. TaWIN2 is a member of 14-3-3 protein family
	CAA72384.1 Y11688 Solanum tuberosum DESCRIPTION: 14-3-3 protein. 35G
	AAC49893.1 U91725 Nicotiana tabacum DESCRIPTION: 14-3-3 isoform d. T14-3d
	CAA65145.1 X95900 Lycopersicon esculentum DESCRIPTION: 14-3-3 protein. tft1 gene
	AAB09581.1 U70534 Glycine max DESCRIPTION: SGF14B. 14-3-3 related protein

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
442	AAB51393.1 U92651 Brassica oleracea var. botrytis DESCRIPTION: tonoplast intrinsic protein bobTIP26-1. TIP
	BAA12711.1 D84669 Raphanus sativus DESCRIPTION: water channel. VM23. VIP1. gamma-Tip homologue
	AAD39372.1 AF118381 Brassica napus DESCRIPTION: tonoplast intrinsic protein. gamma-TIP2. aquaporin
	BAB12722.1 AB048248 Pyrus communis DESCRIPTION: gamma tonoplast intrinsic protein. Py-gTIP
	CAC01618.1 AJ251652 Medicago truncatula DESCRIPTION: water channel. aquaporin. aqp1
	CAB45653.1 AJ243309 Pisum sativum DESCRIPTION: putative tonoplast intrinsic protein. tip
	AAF78757.1 AF271660 Vitis berlandieri x Vitis rupestris DESCRIPTION: water channel. putative aquaporin TIP3. TIP3. TIP-like protein
	AAF82790.1 AF275315 Lotus japonicus DESCRIPTION: a water-selective transport MIP. water-selective transport intrinsic membrane protein 1. aquaporin; LIMP1
	BAA05017.1 D25534 Oryza sativa DESCRIPTION: gamma-Tip. yk333
	AAA02946.1 L12257 Glycine max DESCRIPTION: putative channel protein. nodulin-26
	AAC04846.1 AF020793 Medicago sativa DESCRIPTION: tonoplast intrinsic protein homolog MSMCP1. msmcp1
	AAG44946.1 AF290619 Nicotiana glauca



Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: putative gamma TIP. MIP3
	AAA02947.1 L12258 Glycine max DESCRIPTION: putative channel protein. nodulin-26
	CAA69353.1 Y08161 Nicotiana tabacum DESCRIPTION: aquaporin 1. aqp1
	AAC09245.1 AF037061 Zea mays DESCRIPTION: tonoplast intrinsic protein. ZmTIP1. water channel protein; aquaporin
	AAB17284.1 U43291 Mesembryanthemum crystallinum DESCRIPTION: tonoplast intrinsic protein. TIP. water channel protein
	AAD10494.1 U86762 Triticum aestivum DESCRIPTION: gamma-type tonoplast intrinsic protein. gamma-TIP
	CAA56553.1 X80266 Hordeum vulgare DESCRIPTION: gamma-TIP-like protein
	CAB61841.1 AJ242805 Sporobolus stapfianus DESCRIPTION: putative gamma tonoplast intrinsic protein (TIP)
	AAK26767.1 AF326500 Zea mays DESCRIPTION: tonoplast membrane integral protein ZmTIP1-2
	CAA64952.1 X95650 Tulipa gesneriana DESCRIPTION: tonoplast intrinsic protein. tip1
	AAD31847.1 AF133531 Mesembryanthemum crystallinum DESCRIPTION: water channel protein MipI. MipI
	CAB39758.1 AJ133748 Picea abies DESCRIPTION: putative water channel. major intrinsic protein. mipfg. aquaporin-like protein
	CAA06335.1 AJ005078 Picea abies

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: aquaporin-like protein. MIPr
	AAB51394.1 U92652 Brassica oleracea var. botrytis DESCRIPTION: tonoplast intrinsic protein bobTIP26-2. TIP
	AAG44945.1 AF290618 Nicotiana glauca DESCRIPTION: putative delta TIP. MIP2
	CAB55837.1 AJ245953 Spinacia oleracea DESCRIPTION: putative aquaporin. delta tonoplast intrinsic protein. dtip. highly expressed in leaf, petiole and root and not in epidermal and meristematic cells
	AAB04557.1 U62778 Gossypium hirsutum DESCRIPTION: delta-tonoplast intrinsic protein. delta-TIP
	CAA65185.1 X95951 Helianthus annuus DESCRIPTION: aquaporin
	AAF78758.1 AF271661 Vitis berlandieri x Vitis rupestris DESCRIPTION: water channel. putative aquaporin TIP1. TIP1
	AAD31848.1 AF133532 Mesembryanthemum crystallinum DESCRIPTION: water channel protein MipK. MipK
	CAB95746.2 AJ289866 Vitis vinifera DESCRIPTION: water chanel. putative aquaporin. delta-TIP
	AAB23597.2 S45406 Nicotiana tabacum DESCRIPTION: root-specific gene regulator. TobRB7. This sequence comes from Fig. 1; conceptual translation presented here differs from translation in publication; mismatches (11,13,48,76,83,95,103,197) gap (248-250).
	CAA38634.1 X54855 Nicotiana tabacum DESCRIPTION: possible membrane channel protein
	CAA65184.1 X95950 Helianthus annuus

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: aquaporin
	AAB53329.1 U95008 Lycopersicon esculentum DESCRIPTION: Rb7. RB7. putative water channel protein
	AAC39480.1 AF047173 Vernicia fordii DESCRIPTION: aquaporin
	AAB67881.1 U65700 Solanum tuberosum DESCRIPTION: membrane channel protein. potRB7. putative
	CAA49854.1 X70417 Antirrhinum majus DESCRIPTION: integral membrane protein
	BAA08107.1 D45077 Cucurbita sp. DESCRIPTION: MP23 precursor
	BAA19129.1 AB000506 Daucus carota DESCRIPTION: similar to EMBL Accession Number : X54855
	CAA65187.1 X95953 Helianthus annuus DESCRIPTION: aquaporin. root specific; homologue to TobRb7
	AAK26769.1 AF326502 Zea mays DESCRIPTION: tonoplast membrane integral protein ZmTIP2-2
	AAD10495.1 U86763 Triticum aestivum DESCRIPTION: delta-type tonoplast intrinsic protein. delta-TIP
	BAA31452.1 AB010416 Raphanus sativus DESCRIPTION: water channel of vacuolar membrane; The function a Xenopus oocyte system. delta-VM23. VIP3. a homolog of delta-TIP
	CAA65186.1 X95952 Helianthus annuus DESCRIPTION: aquaporin
	BAA08108.1 D45078 Cucurbita sp. DESCRIPTION: MP28
443	AAA33710.1 L16977 Petunia x hybrida

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: glutamate decarboxylase. gad
	AAA33709.1 L16797 Petunia x hybrida DESCRIPTION: glutamate decarboxylase. gad
	AAB40608.1 U54774 Nicotiana tabacum DESCRIPTION: glutamate decarboxylase. NtGAD1. calmodulin regulated enzyme; calmodulin-binding protein
	AAK18620.1 AF352732 Nicotiana tabacum DESCRIPTION: converts glutamate to gamma-aminobutyric acid. Glutamate decarboxylase isozyme 3. GAD; GAD3; NtGAD3; calcium/calmodulin-dependent enzyme
	AAC24195.1 AF020425 Nicotiana tabacum DESCRIPTION: calmodulin binding protein. glutamate decarboxylase isozyme 1. NtGAD1. calcium-calmodulin-dependent enzyme
	AAC39483.1 AF020424 Nicotiana tabacum DESCRIPTION: glutamate decarboxylase isozyme 2. NtGAD2. calcium-calmodulin-dependent enzyme
	BAB32868.1 AB056060 Oryza sativa DESCRIPTION: glutamate decarboxylase. GAD
	BAB32870.1 AB056062 Oryza sativa DESCRIPTION: glutamate decarboxylase. GAD
	CAA56812.1 X80840 Lycopersicon esculentum DESCRIPTION: homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon
	BAB32869.1 AB056061 Oryza sativa DESCRIPTION: glutamate decarboxylase. GAD
	BAB32871.1 AB056063 Oryza sativa

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: glutamate decarboxylase. GAD
444	AAB69871.1 AF016897 Oryza sativa DESCRIPTION: GDP dissociation inhibitor protein OsGDI2. OsGDI2. GDP dissociation inhibitor2
	CAA06731.1 AJ005836 Cicer arietinum DESCRIPTION: GDP dissociation inhibitor. gdi
	AAB69870.1 AF016896 Oryza sativa DESCRIPTION: GDP dissociation inhibitor protein OsGDI1. OsGDI1. GDP dissociation inhibitor1
446	AAC49716.1 U55035 Brassica rapa DESCRIPTION: small GTP-binding protein Bsarl1a. bsarl1a
	AAC32610.1 AF084005 Avena fatua DESCRIPTION: ras-like small monomeric GTP-binding protein. SAR1. SAR1p
	AAC05127.1 AF048825 Malus x domestica DESCRIPTION: GTP-binding protein Sar1
	AAF17254.1 AF210431 Nicotiana tabacum DESCRIPTION: small GTP-binding protein Sar1BNt
	BAA13463.1 D87821 Nicotiana tabacum DESCRIPTION: NtSar1 protein. NtSAR1
	BAA84612.1 AP000492 Oryza sativa DESCRIPTION: ESTs AU078117(E1380),C72293(E1380) correspond to a region of the predicted gene. similar to SAR1/GTP- binding secretory factor. (AF001308)
	CAA69699.1 Y08423 Nicotiana glauca DESCRIPTION: small GTP-binding protein
	AAC49717.1 U55036 Brassica rapa DESCRIPTION: small GTP-binding protein Bsarl1b. bsarl1b

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	AAA34168.1 L12051 Lycopersicon esculentum DESCRIPTION: GTPase. SAR2
	CAA69700.1 Y08424 Nicotiana plumbaginifolia DESCRIPTION: small GTP-binding protein
	CAA66610.1 X97967 Nicotiana tabacum DESCRIPTION: GTP-binding protein. SAR1
447	AAB69871.1 AF016897 Oryza sativa DESCRIPTION: GDP dissociation inhibitor protein OsGDI2. OsGDI2. GDP dissociation inhibitor2
	AAB69870.1 AF016896 Oryza sativa DESCRIPTION: GDP dissociation inhibitor protein OsGDI1. OsGDI1. GDP dissociation inhibitor1
	CAA06731.1 AJ005836 Cicer arietinum DESCRIPTION: GDP dissociation inhibitor. gdi
	AAB80717.1 AF012823 Nicotiana tabacum DESCRIPTION: inhibits dissociation of GDP from GTP binding proteins. GDP dissociation inhibitor. GDI
449	AAB03108.1 U55032 Brassica napus DESCRIPTION: aspartic protease. protease
	CAA54478.1 X77260 Brassica oleracea DESCRIPTION: aspartic protease. putative
	CAA56373.1 X80067 Brassica oleracea DESCRIPTION: putative aspartic protease
	BAA06875.1 D32144 Oryza sativa DESCRIPTION: aspartic protease
	BAA06876.1 D32165 Oryza sativa DESCRIPTION: aspartic protease
	CAA39602.1 X56136 Hordeum vulgare

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: aspartic proteinase. includes put. pre- and pro-sequences, cleavage sites not determined
	CAA61253.1 X88774 Brassica oleracea DESCRIPTION: aspartic protease. putative
450	CAA56590.1 X80362 Brassica juncea DESCRIPTION: S-adenosyl-L-methionine synthetase. msams
	AAK29409.1 AF346305 Elaeagnus umbellata DESCRIPTION: S-adenosyl-L-methionine synthetase. SAMS1
	AAK29410.1 AF346306 Elaeagnus umbellata DESCRIPTION: S-adenosyl-L-methionine synthetase. SAMS2
	CAA95856.1 Z71271 Catharanthus roseus DESCRIPTION: L-methionine + ATP = S-adenosyl-L-methionine + PPi + Pi. S-adenosyl-L-methionine synthetase 1. CRSAMS1. functional expression in Escherichia coli
	CAA80865.1 Z24741 Lycopersicon esculentum DESCRIPTION: S-adenosyl-L-methionine synthetase
	AAG42490.1 AF321001 Suaeda maritima subsp. salsa DESCRIPTION: S-adenosylmethionine sythetase 2
	CAA80866.1 Z24742 Lycopersicon esculentum DESCRIPTION: S-adenosyl-L-methionine synthetase
	CAA95857.1 Z71272 Catharanthus roseus DESCRIPTION: L-Methionine + ATP = S-adenosyl-L-methionine + PPi + Pi. S-adenosyl-L-methionine synthetase 2. CRSAMS2. functional expression of in Escherichia coli
	AAD48485.1 AF170798 Petunia x hybrida DESCRIPTION: S-adenosyl-L-methionine synthetase
	AAD56396.1 AF183891 Petunia x hybrida DESCRIPTION: S-adenosyl-L-methionine synthetase. sam2

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	AAG17666.1 AF271220 Brassica juncea DESCRIPTION: S-adenosylmethionine synthetase. MSAMS2
	CAA95858.1 Z71273 Catharanthus roseus DESCRIPTION: L-methionine + ATP = S-adenosyl-L-methionine + PPi + Pi. S-adenosyl-L-methionine synthetase 3. CRSAMS3. functional expression in Escherichia coli
	CAA81481.1 Z26867 Oryza sativa DESCRIPTION: S-adenosyl methionine synthetase
	BAA96637.1 AP002482 Oryza sativa DESCRIPTION: Similar to Oryza sativa S-adenosylmethionine synthetase 1 (P46611)
	AAA79831.1 U38186 Pinus banksiana DESCRIPTION: S-adenosyl methionine synthetase
	AAG17036.1 AF187821 Pinus contorta DESCRIPTION: catalyzes the reaction between methionine and ATP to S-adenosylmethionine. S-adenosylmethionine synthetase. sams2
	CAB83039.1 AJ277206 Camellia sinensis DESCRIPTION: s-adenosylmethionine synthetase
	BAA94605.1 AB041534 Camellia sinensis DESCRIPTION: s-adenosylmethionine synthetase. SAM
	AAA81377.1 U17239 Actinidia chinensis DESCRIPTION: S-adenosylmethionine synthetase
	AAB38500.1 U79767 Mesembryanthemum crystallinum DESCRIPTION: S-adenosylmethionine synthetase. methionine adenosyltransferase
	AAA81378.1 U17240 Actinidia chinensis DESCRIPTION: S-adenosylmethionine synthetase



Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	CAA80867.1 Z24743 Lycopersicon esculentum DESCRIPTION: S-adenosyl-L-methionine synthetase
	AAF42974.1 AF127243 Nicotiana tabacum DESCRIPTION: S-adenosyl-L-methionine synthetase. SAMS
	CAA57696.1 X82214 Petunia x hybrida DESCRIPTION: methionine adenosyltransferase. sam1
	AAA20112.1 M73430 Populus x generosa DESCRIPTION: S-adenosyl methionine synthetase
	AAC05590.1 U82833 Oryza sativa DESCRIPTION: S-adenosyl-L-methionine synthetase. pOS-SAMS2
	AAB71138.1 AF004317 Musa acuminata DESCRIPTION: S-adenosyl-L-methionine synthetase homolog
	BAA09895.1 D63835 Hordeum vulgare DESCRIPTION: S-adenosylmethionine synthetase
	AAA33274.1 M61882 Dianthus caryophyllus DESCRIPTION: S-adenosylmethionine synthetase. CARSAM2
	CAA57581.1 X82077 Pisum sativum DESCRIPTION: methionine adenosyltransferase. SAMs2
	AAA58773.1 L36681 Pisum sativum DESCRIPTION: S-adenosylmethionine synthase. precursor for ethylene and polyamine biosynthesis
	AAA58772.1 L36680 Pisum sativum DESCRIPTION: precursor for ethylene and polyamine biosynthesis. S-adenosylmethionine synthase
	CAA57580.1 X82076 Pisum sativum DESCRIPTION: methionine adenosyltransferase. SAMs1

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	AAA81379.1 U17241 Actinidia chinensis DESCRIPTION: S-adenosylmethionine synthetase
	AAA33857.1 M62758 Petroselinum crispum DESCRIPTION: S-adenosylmethionine synthetase. SMS-1
	AAB71833.1 AF008568 Chlamydomonas reinhardtii DESCRIPTION: S-adenosylmethionine synthetase. CHRSAMS
	AAA33858.1 M62757 Petroselinum crispum DESCRIPTION: S-adenosylmethionine synthetase. SMS-2
	AAA73483.1 U27348 Populus deltoides DESCRIPTION: S-adenosyl-L-methionine synthetase. Sam1
	BAA21726.1 AB006187 Nicotiana tabacum DESCRIPTION: S-adenosylmethionine synthase. BYJ90
	CAA65455.1 X96680 Catharanthus roseus DESCRIPTION: methionine adenosyltransferase. SAM1
	CAA59508.1 X85252 Cicer arietinum DESCRIPTION: SAM-synthetase. SAMs.
	AAF78525.1 AF195233 Pyrus pyrifolia DESCRIPTION: S-adenosylmethionine synthase. SAMS
454	AAA34046.1 M83940 Spinacia oleracea DESCRIPTION: 10-formyltetrahydrofolate synthetase. sfs1
465	CAA64455.1 X94999 Mesembryanthemum crystallinum DESCRIPTION: V-type ATPase c subunit. Vmac1
	AAC49473.1 U16244 Kalanchoe daigremontiana DESCRIPTION: V-type H <sup>+</sup> -ATPase 16 kDa subunit. c subunit, presumed H <sup>+</sup> conducting pore of vacuolar-type H <sup>+</sup> ATPase; integral membrane protein, localized to vacuole and possibly other endomembranes
	AAA82977.1 U13670 Gossypium hirsutum

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: vacuolar H <sup>+</sup> -ATPase proteolipid (16 kDa) subunit. cval6-4
	AAA82976.1 U13669 Gossypium hirsutum DESCRIPTION: vacuolar H <sup>+</sup> -ATPase proteolipid (16 kDa) subunit. cval6-2
	CAA67356.1 X98851 Beta vulgaris DESCRIPTION: proton channel, proteolipid. subunit c of V-type ATPase
	BAA89595.1 AB036923 Citrus unshiu DESCRIPTION: vacuolar H <sup>+</sup> -ATPase c subunit. Cit-VATP c-2
	BAA89594.1 AB036922 Citrus unshiu DESCRIPTION: vacuolar H <sup>+</sup> -ATPase c subunit. Cit-VATP c-1.
	BAA75542.1 AB024275 Citrus unshiu DESCRIPTION: protein translocation. vacuolar H <sup>+</sup> -ATPase c subunit. CitVATP c-2
	BAA75515.1 AB024274 Citrus unshiu DESCRIPTION: protein translocation. vacuolar H <sup>+</sup> -ATPase c subunit. CitVATP c-1
	AAC12797.1 AF022925 Vigna radiata DESCRIPTION: adenosine triphosphatase. c-subunit of V-ATPase
	AAF04597.1 AF193814 Dendrobium crumenatum DESCRIPTION: vacuolar H <sup>+</sup> -ATP synthase 16kDa proteolipid subunit. V-ATPase subunit
	AAC12798.1 AF022926 Vigna radiata DESCRIPTION: adenosine triphosphatase. c-subunit of V-ATPase
	BAA89596.1 AB036924 Citrus unshiu DESCRIPTION: vacuolar H <sup>+</sup> -ATPase c subunit. Cit-VATP c-3
	BAA75516.1 AB024276 Citrus unshiu

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: protein translocation. vacuolar H <sup>+</sup> -ATPase c subunit. CitVATP c-3
	AAK01292.1 AF331709 <i>Avicennia marina</i> DESCRIPTION: vacuolar ATPase subunit c. V-ATPase subunit c
	CAA65062.1 X95751 <i>Nicotiana tabacum</i> DESCRIPTION: proteolipid, proton channel. c subunit of V-type ATPase. isoform 1
	AAB64199.1 AF010228 <i>Lycopersicon esculentum</i> DESCRIPTION: vacuolar proton ATPase proteolipid subunit. LVA-P1; induced by gibberellin
	AAA68175.1 U27098 <i>Oryza sativa</i> DESCRIPTION: H <sup>+</sup> -ATPase. vatp-P1
	CAA71930.1 Y11037 <i>Beta vulgaris</i> DESCRIPTION: BV-16/1
	CAA65063.1 X95752 <i>Nicotiana tabacum</i> DESCRIPTION: proteolipid, proton channel. c subunit of V-type ATPase. isoform 2
	AAA32712.1 M73232 <i>Avena sativa</i> DESCRIPTION: H <sup>+</sup> -ATPase. vatp-P1
	BAA23351.1 AB003941 <i>Acetabularia acetabulum</i> DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA23352.1 AB003942 <i>Acetabularia acetabulum</i> DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA23350.1 AB003940 <i>Acetabularia acetabulum</i> DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA21683.1 AB003938 <i>Acetabularia acetabulum</i> DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA21682.1 AB003937 <i>Acetabularia acetabulum</i>

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA23349.1 AB003939 Acetabularia acetabulum DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	CAA63118.1 X92374 Zea mays DESCRIPTION: V-type H <sup>+</sup> -ATPase. subunit C
	CAA63119.1 X92375 Zea mays DESCRIPTION: V-type H <sup>+</sup> -ATPase. subunit C
466	BAA21682.1 AB003937 Acetabularia acetabulum DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA23349.1 AB003939 Acetabularia acetabulum DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	AAF04597.1 AF193814 Dendrobium crumenatum DESCRIPTION: vacuolar H <sup>+</sup> -ATP synthase 16kDa proteolipid subunit. V-ATPase subunit
	AAC12798.1 AF022926 Vigna radiata DESCRIPTION: adenosine triphosphatase. c-subunit of V-ATPase
	AAC12797.1 AF022925 Vigna radiata DESCRIPTION: adenosine triphosphatase. c-subunit of V-ATPase
	CAA64455.1 X94999 Mesembryanthemum crystallinum DESCRIPTION: V-type ATPase c subunit. Vmac1
	AAC49473.1 U16244 Kalanchoe daigremontiana DESCRIPTION: V-type H <sup>+</sup> -ATPase 16 kDa subunit. c subunit, presumed H <sup>+</sup> conducting pore of vacuolar-type H <sup>+</sup> ATPase; integral membrane protein, localized to vacuole and possibly other endomembranes
	AAA82977.1 U13670 Gossypium hirsutum DESCRIPTION: vacuolar H <sup>+</sup> -ATPase proteolipid (16 kDa) subunit. cva16-4

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	AAA82976.1 U13669 <i>Gossypium hirsutum</i> DESCRIPTION: vacuolar H <sup>+</sup> -ATPase proteolipid (16 kDa) subunit. cva16-2
	CAA67356.1 X98851 <i>Beta vulgaris</i> DESCRIPTION: proton channel, proteolipid. subunit c of V-type ATPase
	BAA89595.1 AB036923 <i>Citrus unshiu</i> DESCRIPTION: vacuolar H <sup>+</sup> -ATPase c subunit. Cit-VATP c-2
	BAA89594.1 AB036922 <i>Citrus unshiu</i> DESCRIPTION: vacuolar H <sup>+</sup> -ATPase c subunit. Cit-VATP c-1
	BAA75542.1 AB024275 <i>Citrus unshiu</i> DESCRIPTION: protein translocation. vacuolar H <sup>+</sup> -ATPase c subunit. CitVATP c-2
	BAA89596.1 AB036924 <i>Citrus unshiu</i> DESCRIPTION: vacuolar H <sup>+</sup> -ATPase c subunit. Cit-VATP c-3
	BAA75516.1 AB024276 <i>Citrus unshiu</i> DESCRIPTION: protein translocation. vacuolar H <sup>+</sup> -ATPase c subunit. CitVATP c-3
	AAK01292.1 AF331709 <i>Avicennia marina</i> DESCRIPTION: vacuolar ATPase subunit c. V-ATPase subunit c
	AAB64199.1 AF010228 <i>Lycopersicon esculentum</i> DESCRIPTION: vacuolar proton ATPase proteolipid subunit. LVA-P1; induced by gibberellin
	CAA65062.1 X95751 <i>Nicotiana tabacum</i> DESCRIPTION: proteolipid, proton channel. c subunit of V-type ATPase. isoform 1
	CAA71930.1 Y11037 <i>Beta vulgaris</i> DESCRIPTION: BV-16/1

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	AAA68175.1 U27098 Oryza sativa DESCRIPTION: H <sup>+</sup> -ATPase. vatp-P1
	CAA65063.1 X95752 Nicotiana tabacum DESCRIPTION: proteolipid, proton channel. c subunit of V-type ATPase. isoform 2
	AAA32712.1 M73232 Avena sativa DESCRIPTION: H <sup>+</sup> -ATPase. vatp-P1
	BAA23352.1 AB003942 Acetabularia acetabulum DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA23350.1 AB003940 Acetabularia acetabulum DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA21683.1 AB003938 Acetabularia acetabulum DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	BAA23351.1 AB003941 Acetabularia acetabulum DESCRIPTION: vacuolar type H <sup>+</sup> -ATPase proteolipid subunit
	CAA63118.1 X92374 Zea mays DESCRIPTION: V-type H <sup>+</sup> -ATPase. subunit C
	CAA63119.1 X92375 Zea mays DESCRIPTION: V-type H <sup>+</sup> -ATPase. subunit C
467	AAD56018.1 AF180758 Vitis riparia DESCRIPTION: 60S ribosomal protein L10. QM. similar to QM family proteins
	AAG27431.1 AF295636 Elaeis guineensis DESCRIPTION: QM-like protein. tumor supressor protein
	AAF34765.1 AF227620 Euphorbia esula DESCRIPTION: 60S ribosomal protein L10. belongs to the L10E family of ribosomal proteins
	BAA19462.1 AB001891 Solanum melongena

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: QM family protein. EQM
	AAB66347.1 AF013804 Pinus taeda DESCRIPTION: Wilm's tumor supressor homolog. lp20. LP20
	AAA17419.1 U06108 Zea mays DESCRIPTION: QM protein
	AAA98698.1 U55048 Oryza sativa DESCRIPTION: QM. similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex subunit VI requiring protein SC34
	CAA57339.1 X81691 Oryza sativa DESCRIPTION: putative tumor suppresser. SC34
	CAA57340.1 X81692 Oryza sativa DESCRIPTION: putative tumor supressor. SG12
	AAG17477.1 AF106846 Oryza sativa DESCRIPTION: QM protein
	AAA99158.1 U55212 Oryza sativa DESCRIPTION: putative tumor suppressor. Wilms' tumor-related protein QM
	CAA78461.1 Z14083 Nicotiana tabacum DESCRIPTION: HOMOLOGIE with Human WILM's tumor-related protein HUMQM
	BAA19414.1 AB001582 Solanum melongena DESCRIPTION: QM family protein. TM002
527	CAA52414.1 X74403 Phaseolus vulgaris DESCRIPTION: cyclophilin. Cyp
	CAA69622.1 Y08320 Digitalis lanata DESCRIPTION: cyclophylin
	BAA25755.1 AB012947 Vicia faba



Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	DESCRIPTION: vcCyP
	CAA69598.1 Y08273 <i>Digitalis lanata</i> DESCRIPTION: cyclophilin. CYP18
	CAA59468.1 X85185 <i>Catharanthus roseus</i> DESCRIPTION: cyclophilin. PCKR1
	CAA76054.1 Y16088 <i>Lupinus luteus</i> DESCRIPTION: cytosolic form of cyclophilin
	AAF00471.1 AF178458 <i>Lupinus luteus</i> DESCRIPTION: cytosolic cyclophilin. CYCLOPH
	AAA63543.1 M55019 <i>Lycopersicon esculentum</i> DESCRIPTION: cyclophilin. CyP. the published citation gene name is 'CyP', but the submission gene name is 'Rot1'
	AAD22975.1 AF126551 <i>Solanum tuberosum</i> subsp. <i>tuberosum</i> DESCRIPTION: cyclophilin. cytosolic; peptidyl-prolyl cis-trans isomerase; Cyp; PPIase; romatase
	AAA62706.1 M55018 <i>Brassica napus</i> DESCRIPTION: cyclophilin. CyP. The published citation gene name is 'CyP', but the author submission gene name is 'Rot1'
	AAF65770.1 AF242312 <i>Euphorbia esula</i> DESCRIPTION: accelerate protein folding. cyclophilin. peptidyl-prolyl cis-trans isomerase; PPIASE
	CAA48638.1 X68678 <i>Zea mays</i> DESCRIPTION: peptidyl-prolyl cis-trans isomerase. cyclophilin
	AAA63403.1 M55021 <i>Zea mays</i> DESCRIPTION: cyclophilin. CyP. the published citation gene name is 'CyP', but the submission gene name is 'Rot1'
	AAB51386.1 U92087 <i>Solanum commersonii</i> DESCRIPTION: stress responsive cyclophilin. SCCYP1

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	AAA57045.1 L29469 Oryza sativa DESCRIPTION: cyclophilin 2. Cyp2
	AAA57046.1 L29470 Oryza sativa DESCRIPTION: cyclophilin 2. Cyp2
	AAC05639.1 AF052206 Chlamydomonas reinhardtii DESCRIPTION: cyclophilin 1. cyp1. immunophilin; peptidyl prolyl isomerase
	AAA57044.1 L29471 Oryza sativa DESCRIPTION: cyclophilin 1. Cyp1
	AAA32642.1 L13365 Allium cepa DESCRIPTION: cyclophilin. CyP. putative
	AAG01536.1 AF291180 Capsicum annuum DESCRIPTION: cyclophilin CACYP1
	AAA64430.1 L32095 Vicia faba DESCRIPTION: cyclophilin
	AAG03106.1 AC073405 Oryza sativa DESCRIPTION: similar to Arabidopsis thaliana Peptidyl-prolyl cis-trans isomerase (P34791). 3' incomplete
	CAA10766.1 AJ132763 Pseudotsuga menziesii DESCRIPTION: catalyze the cis-trans isomerization of proline peptide bonds. cyclophilin
528	AAB69871.1 AF016897 Oryza sativa DESCRIPTION: GDP dissociation inhibitor protein OsGDI2. OsGDI2. GDP dissociation inhibitor2
	AAB69870.1 AF016896 Oryza sativa DESCRIPTION: GDP dissociation inhibitor protein OsGDI1. OsGDI1. GDP dissociation inhibitor1

Arabidopsis ORF (SEQ ID NO)	Homologous sequence
	CAA06731.1 AJ005836 Cicer arietinum DESCRIPTION: GDP dissociation inhibitor. gdi
	AAB80717.1 AF012823 Nicotiana tabacum DESCRIPTION: inhibits dissociation of GDP from GTP binding proteins. GDP dissociation inhibitor. GDI
529	AAB99756.1 AF020272 Medicago sativa DESCRIPTION: malate dehydrogenase. cmdh
	AAB64290.1 AF007581 Zea mays DESCRIPTION: cytoplasmic malate dehydrogenase
	AAK26431.1 AF353203 Oryza sativa DESCRIPTION: cytoplasmic malate dehydrogenase. oxidoreductase
	AAG13573.1 AC037425 Oryza sativa DESCRIPTION: cytoplasmic malate dehydrogenase. OSJNBa0055P24.3
	CAA65384.1 X96539 Mesembryanthemum crystallinum DESCRIPTION: malate dehydrogenase. mdh
	CAB61618.1 AJ251083 Beta vulgaris DESCRIPTION: putative malate dehydrogenase. putative cytosolic malate dehydrogenase. nr1.
	CAC12826.1 AJ299256 Nicotiana tabacum DESCRIPTION: malate dehydrogenase. md1

**What is claimed is:**

1. An isolated polynucleotide comprising a plant nucleotide sequence that directs root-specific transcription of an operatively linked nucleic acid segment in a plant cell, which plant nucleotide sequence is from a gene encoding a polypeptide that is substantially  
5 similar to a polypeptide encoded by an *Arabidopsis* gene comprising a promoter selected from the group consisting of SEQ ID NOs:1-51, 518-526, and 536-544 or a polypeptide encoded by an *Oryza* gene comprising a promoter selected from the group consisting of SEQ ID NO:825 and 843.
- 10 2. An isolated polynucleotide comprising a plant nucleotide sequence that directs root-specific transcription of an operatively linked nucleic acid segment in a plant cell, which plant nucleotide sequence hybridizes under high stringency conditions to the complement of any one of SEQ ID NOs:1-51, 518-526, 536-544, 825 and 843.
- 15 3. An isolated polynucleotide comprising a plant nucleotide sequence that directs root-specific transcription of an operatively linked nucleic acid segment in a plant cell which plant nucleotide sequence hybridizes under very high stringency conditions to the complement of any one of SEQ ID NOs:1-51, 518-526, 536-544, 825 and 843.
- 20 4. An isolated polynucleotide comprising a plant nucleotide sequence that directs root-specific transcription of an operatively linked nucleic acid segment in a plant cell which plant nucleotide sequence is selected from the group consisting of SEQ ID NOs:1-51, 518-526, 536-544, 825 and 843 or a fragment thereof.
- 25 5. An isolated polynucleotide comprising a plant nucleotide sequence that directs constitutive transcription of an operatively linked nucleic acid segment in a plant cell, which plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an *Arabidopsis* gene comprising a promoter selected from the group consisting of SEQ ID NOs:52-339, 477-515, 517,  
30 545-579, 826-842 and 844-875.

6. An isolated polynucleotide comprising a plant nucleotide sequence that directs constitutive transcription of an operatively linked nucleic acid segment in a plant cell, which plant nucleotide sequence hybridizes under high stringency conditions to the complement of any one of SEQ ID NOs:52-339, 477-515, 517, 545-579, 826-842 and 844-875.
7. An isolated polynucleotide comprising a plant nucleotide sequence that directs constitutive transcription of an operatively linked nucleic acid segment in a plant cell which plant nucleotide sequence hybridizes under very high stringency conditions to the complement of any one of SEQ ID NOs:52-339, 477-515, 517, 545-579, 826-842 and 844-875.
8. An isolated polynucleotide comprising a plant nucleotide sequence that directs constitutive transcription of an operatively linked nucleic acid segment in a plant cell which plant nucleotide sequence is selected from the group consisting of SEQ ID NOs:52-339, 477-515, 517, 545-579, 826-842 and 844-875 or a fragment thereof.
9. An isolated polynucleotide comprising a plant nucleotide sequence that directs leaf-specific transcription of an operatively linked nucleic acid segment in a plant, which plant nucleotide sequence is from a gene encoding a polypeptide that is substantially similar to a polypeptide encoded by an *Arabidopsis* gene having a promoter selected from the group consisting of SEQ ID NOs: 693-773.
10. An isolated polynucleotide comprising a plant nucleotide sequence that directs leaf-specific transcription of an operatively linked nucleic acid segment in a plant cell, which plant nucleotide sequence that hybridizes under high stringency conditions to the complement of any one of SEQ ID NOs: 693-773.
11. An isolated polynucleotide comprising a plant nucleotide sequence that directs leaf-specific transcription of an operatively linked nucleic acid segment in a plant cell, which

plant nucleotide sequence hybridizes under very high stringency condition to the complement of any one of SEQ ID NOs: 693-773.

12. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which plant nucleotide sequence is selected from the group consisting of SEQ ID NOs: 693-773 or a fragment thereof.
13. The polynucleotide of any one of claims 1 to 12 wherein the plant nucleotide sequence is 25 to 2000 nucleotides in length.
14. The polynucleotide of any one of claims 1, 5 or 9 wherein the plant nucleotide sequence has at least 80% nucleotide sequence identity to one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, 693-773 and 825-875.
15. The polynucleotide of any one of claims 1, 5 or 9 wherein the plant nucleotide sequence has at least 90% nucleotide sequence identity to one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, 693-773 and 825-875.
16. The polynucleotide of any one of claims 1, 5 or 9 wherein the plant nucleotide sequence has at least 98% nucleotide sequence identity to one of SEQ ID NOs: 1-339, 477-515, 517-526, 536-579, 693-773 and 825-875.
17. The polynucleotide of any one of claims 1 to 3, 5 to 7, 9 to 11, and 13 to 16 wherein the plant nucleotide sequence is from a dicot.
18. The polynucleotide of any one of claims 1 to 3, 5 to 7, 9 to 11, and 13 to 16 wherein the plant nucleotide sequence is from a monocot.

19. The polynucleotide of any one of claims 1 to 3, 5 to 7, 9 to 11, and 13 to 16 wherein the plant nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.
- 5 20. The polynucleotide of any one of claims 1 to 19 which comprises a TATA box, a CAAT box, or both.
21. A composition comprising the polynucleotide of any one of claims 1 to 20.
- 10 22. A recombinant vector comprising the polynucleotide of any one of claims 1 to 20.
23. The vector of claim 22 which is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor and phage.
- 15 24. An expression cassette comprising the polynucleotide of any one of claims 1 to 20 operatively linked to an open reading frame.
25. The expression cassette of claim 24 operably linked to other suitable regulatory sequences.
- 20 26. The expression cassette of claim 24 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which directs transcription.
27. The expression cassette of claim 24 wherein the open reading frame is in a sense orientation relative to the nucleotide sequence which directs transcription.
- 25 28. A recombinant vector comprising the expression cassette of claim 24.
29. The vector of claim 28 wherein the vector is selected from the group consisting of a plasmid, phagemid, cosmid, virus, F-factor or phage.
- 30

30. A host cell comprising the expression cassette of claim 24.
31. The host cell of claim 30 wherein the cell is selected from the group consisting of a yeast, a bacterium, a cereal plant cell, and an *Arabidopsis* cell.
- 5 32. A plant cell containing the expression cassette of claim 24.
33. The plant cell of claim 32 which is a monocot cell.
- 10 34. The plant cell of claim 32 which is a dicot cell.
35. A transformed plant, the genome of which is augmented with the expression cassette of claim 24.
- 15 36. A transformed plant comprising transformed plant cells, which cells contain the expression cassette of claim 24.
37. The transformed plant of claim 35 or 36 which is a dicot.
- 20 38. The transformed plant of claim 35 or 36 which is a monocot.
39. The transformed plant of claim 35 or 36 which is selected from the group consisting of maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice, wheat and *Arabidopsis*.
- 25 40. A method for augmenting a plant genome, comprising:
- a) contacting plant cells with the expression cassette of claim 24 so as to yield a transformed plant cell; and
- b) regenerating the transformed plant cell to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.
- 30



41. A transformed plant prepared by the method of claim 40.
42. A product of the plant of claim 41 which comprises the expression cassette or the gene  
5 product encoded by the open reading frame.
43. The product of claim 42 which is selected from the group consisting of a seed, fruit,  
vegetable, transgenic plant, and a progeny plant.
- 10 44. A plant cell comprising the vector of claim 28.
45. The plant cell of claim 44 which is a dicot cell.
46. The plant cell of claim 44 which is a monocot cell.
- 15 47. The plant cell of claim 44 which is a cereal cell.
48. A transformed plant, the cells of which comprise the vector of claim 28.
- 20 49. The plant of claim 48 which is a cereal plant.
50. The plant claim 48 which is a dicot.
51. The plant of claim 48 which is a monocot.
- 25 52. The plant of claim 48 which is selected from the group consisting of a maize, soybean,  
barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco,  
sugarbeet, rice, wheat and *Arabidopsis* plant.
- 30 53. A method to identify a gene having a promoter, the expression of which is altered in  
root comprising:

- 5           a)   contacting a plurality of isolated nucleic acid samples on a solid substrate with  
            a probe comprising plant nucleic acid corresponding to RNA isolated from root  
            so as to form a complex, wherein each sample comprises a plurality of  
            oligonucleotides corresponding to at least a portion of one plant gene; and  
10          b)   comparing complex formation in a) with complex formation between a second  
            plurality isolated nucleic acid of samples on a solid substrate contacted with a  
            second probe comprising plant nucleic acid corresponding to RNA that is not  
            from root, so as to identify which samples correspond to genes that are  
            expressed in root, wherein the identified genes are orthologs of *Arabidopsis*  
15          genes comprising a promoter selected from the group consisting of SEQ ID  
            NOs:1-51, 825 and 843.

54.   A method to identify a gene having a promoter, the expression of which is constitutive  
in a plant cell, comprising:

- 15          a)   contacting a plurality of isolated nucleic acid samples on a solid substrate with a  
            probe comprising plant nucleic acid corresponding to RNA isolated from two  
            or more tissues or at two or more developmental stages of a plant so as to form  
            a complex, wherein each sample comprises a plurality of oligonucleotides  
            corresponding to at least a portion of one plant gene; and  
20          b)   comparing complex formation in the samples so to identify which samples  
            correspond to genes that are expressed in two or more tissues or at two or  
            more developmental stages of the plant, wherein the identified genes are  
            orthologs of *Arabidopsis* genes comprising a promoter selected from the group  
            consisting of SEQ ID NOs:52-339, 826-842 and 844-875.

25

55.   A method to identify a gene having a promoter, the expression of which is altered in  
leaves of a plant, comprising:

- a)   contacting a plurality of isolated nucleic acid samples on a solid substrate with a  
probe comprising plant nucleic acid corresponding to RNA isolated from leaves

of a plant so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and

- b) comparing complex formation in a) to complex formation between a second plurality of isolated nucleic acid samples on a solid substrate contacted with a second probe comprising plant nucleic acid corresponding to plant RNA that is not from leaves of a plant, so as to identify which samples correspond to genes that are expressed in leaves, wherein the identified genes are orthologs of *Arabidopsis* genes comprising a promoter selected from the group consisting of SEQ ID NOs:693-773.

10

56. The method of any one of claims 53 to 55 wherein the probes comprise nucleic acid from a dicot.

15

57. The method of any one of claims 53 to 55 wherein the probes comprise nucleic acid from a monocot.

58. The method of any one of claims 53 to 55 wherein the probes comprise nucleic acid from a cereal plant.

20

59. A method to alter the phenotype of a plant cell comprising: introducing the expression cassette of claim 24 into a plant cell and expressing that open reading frame in the cell so as to alter a characteristic of that cell relative to a plant cell that does not comprise the expression cassette.

25

60. The method of claim 59 wherein the cell is a monocot cell.

61. The method of claim 59 wherein the cell is a dicot cell.

62. The method of claim 59 wherein the cell is a cereal cell.

30

63. The method of claim 59 wherein the open reading frame is a nucleic acid sequence from maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat.
- 5 64. The method of claim 59 wherein the open reading frame is in an antisense orientation relative to the nucleotide sequence which directs transcription.
65. The method of claim 59 wherein the expression inhibits transcription or translation of endogenous plant nucleic acid sequences corresponding to the open reading frame.
- 10 66. The method of claim 59 wherein the open reading frame is in a sense orientation relative to the nucleotide sequence which directs transcription.
67. The method of claim 59, wherein the open reading frame is expressed in an amount that  
15 is greater than the amount in a plant which does not comprise the expression cassette.
68. The method of claim 59 wherein the open reading frame encodes a protein.
69. The method of claim 68 wherein the protein encodes a regulatory product.
- 20 70. The method of claim 68 wherein the protein activates transcription.
71. The method of claim 68 wherein the protein represses transcription.
- 25 72. The method of claim 68 wherein protein confers insect resistance, confers stress-tolerance, or increases nutrient uptake.
73. The method of claim 59 wherein the plant nucleotide sequence is operably linked to an open reading frame from an insect resistance gene, a bacterial disease resistance gene, a  
30 fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a stress resistance gene, a gene affecting

grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, or an environment or stress resistance gene.

5

74. A computer-readable medium having stored thereon a data structure comprising:
- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs:1-339, 457, 476-515, 517-526, 536-579, 602, 693-773 and 825-875 or the complement thereof; and
  - b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

10

75. The computer readable medium of claim 74 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.

15

76. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:
- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-339, 457, 476-515, 517-526, 536-579, 602, 693-773 and 825-875 or the complement thereof; and
  - b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

20

25

77. The computer readable medium of claim 76 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.

30

78. The expression cassette of claim 24 wherein the open reading frame is from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a stress resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, or an environment or stress resistance gene.
- 5
79. The method of claim 73 wherein the stress resistance gene confers resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, excessive salt, or excessive oxidative stress.
- 10
80. The expression cassette of claim 78 wherein the stress resistance gene confers resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, excessive salt, or excessive oxidative stress.
- 15